

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACCGCGTCCGGGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTGCGTCTTCCCG
CAGCGCTACCCGCCATGCGCTGCCGCCGGCGCTGGGGCTCCTGCCGCTTCTGCTG
CTGCTGCCGCCGCCGGAGGCCAAGAAGCCGACGCCCTGCCACCAGGTGCCGGGGCT
GGTGGACAAGTTAACCAAGGGATGGTGACACCGCAAAGAAGAACTTGGCGGGAAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATCGAGTGGTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCCAGTGTCTGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGAGATGGAGCAGACA
GGCGACGGGTCTGCCGGTGCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCGCGAGTGTGAAGTGGCTGGTGCT
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGTGTG
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAAGATGTGGACGAGTGTCACTAGCAGAAAAAAACCTGTGTGAGGAAAAACG
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGTCCTGACGGCTTCGAAGAAACG
GAAGATGCCTGTGCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGGAAGACCTGTAATTGCGGACTTACCCCTAAATTATTAGAAGGATGTCC
CGTGGAAAATGTGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGGGGAGAGGCTGC
CTGCTCTCTAACGGTGATTCTCATTGTCCTTAAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTTGTATATTTGATACAGTTCTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAGGGCGCCGCGACTCTAGAGTCGACCTGCAGAAC
TTGGCCGCCATGGCCAACTTGTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCA
TCACAAATTTCACAAATAAGCATTTCAGCTGATTCTAGTTGTGGTTGTCCAAACTC
ATCAATGTATCTTATCATGTCGGATCGGAATTAAATTGCCGCAGCACCATGGCTGAAAT
AACCTCTGAAAGAGGAACCTGGTAGGTACCTCTGAGGCGAAAGAACCCAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLPPAPEAAKKPTPCHRGRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMILEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLVCCSPGTYGPDCLACQGGSQRPCSG
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNEHTSICTACDESCKTCGTLNRDCGECEVGVLDE
GACVDVDECAAEPVPCSAAQFCKNANGSYTCECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGGTCCAAC TG CACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACCGCGTCCGCCAGGCCGGAGGGCAGCGCCCAGCGTCTAAACGGGAACAA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGGCCAGGTGCGTAGGTGCG
GCACGAGGAGTTTCCCGCAGCGAGGAGGTCTGAGCAGCAGCATGGCCCGAGGAGCGCCTTC
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCTGTGCCTGCTGGCACTGCAGGGCGGAGGC
CGGGCCGCCGCAGGAGAGAGCCTGTACCTATGGATCGATGCTACCAGGCAAGAGTACTCA
TAGGATTGAAGAAGATATCCTGATTGTTCAGAGGGAAAATGGCACCTTACACATGAT
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCATATCCATTCCATGAATTTCAC
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGTCCTGCGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCTCTGCTGGAACAGTGCCCTACAAGGCA
TCAGTTGTTCAAGTTGGTTCCATGTCCTGGAAAACAGGATGGGTGGCAGCATTGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCT
TCTTTAAACATGTCAACAAGCTGAGTCCCAGGCAGGTTGCCGAAATGGAGGCTTTGTAAT
GAAAGACGCATCTGCGAGTGTCTGATGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCCACGATGTATGAATGGTGGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAACCTGTGACAAAGCAAACGCTCAACCACCTGCTTAAATGGAGGGACC
TGTGTTCTACCCCTGGAAAATGTATTGCCCCCTCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCACAACCTGCGAAATGGAGGTAAATGCATTGGTAAAGCAAATGTAAGTGT
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTCACAT
GGAACCTGCCATGAACCCAAACAAATGCCAATGTCAGAAAGGTTGCCATGGAAGACACTGCAA
TAAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGCGCCAGCTCAGGCAGC
ACACGCCCTCACTAAAAAGGCCAGGGAGCGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTCATAGCCTTGTAAACCTTCA
TGTGTTGAATGTTCAAATAATGTTCAATTACACTTAAGAATACTGCCCTGAATTGTTATTAGCT
TCATTATAAATCACTGAGCTGATATTACTCTTCTTTAAGTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTCTTCTGTTCAAGTGTCTGGACAGATTATATTATGTCAATTGA
TCAGGTTAAAATTTCAGTGTGAGTTGCCAGATATTCTAAAATTACAATGCAATTGTT
GTCTGGGGCAGGGAAACATCAGAAAGGTTAAATTGGGAAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTCTAGATTATTGTCAAGATATTAGAT
GTTTGTACATTAAAATTGCTCTTAATTAAACTCTCAATACAATATATTGTCAC
TTACCAATTATTCCAGAGATTCACTGTTGGCAGATATTCTAAAATTACAATGCAATTGTT
AAACAATATAAATATTCTAAACACAATGAAATAGGGAAATAATGTATGAACCTTTGCA
TGGCTTGAAGCAATATAAATATTGTAACAAAACACAGCTCTACCTAATAAACATT
ACTGTTGTATGTATAAAATAAGGTGCTGTTAGTTTTGGAAAAA
AAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCCAACTGTTATTGCAGCTTATAATG

FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
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MAPFTHDFRKAQQRMPAI PVNIHSMNFTWQAAQAEYFYEFLSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCI CPPGLEGEQCEISKCPQPCRNGGKIGKSCKCSKGYQGDLCSPVVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW
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Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGCGTCCGGCGTCGAGAGCCAGGAGGCGGAGGCAGCGCGCGGGCCAGCCTGGG
CCCCAGCCCACACCTCACCAAGGGCCCAGGAGCCACCATGTGGCGATGTCCACTGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGCTCGGGCTGGCCAGCAGGGCTGTGGCGCCGG
GAGCTAGCACCGGGTCTGCACCTGCACGGGATCCGGGACGCACGGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCACTCGGGCGCCATCT
GTTACTGTGACCTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGGCGTGCCACCCCCTTCCCCGATCCAAGGATGTATGCATGGAGGTGCTATCTA
TCCAGTCTGGGAACGTACTGGACAACGTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGGCCCTCTGGGCATGACCCTGGATGAGGGCATTGCTACCGCTGGCACCA
TCCGCCATCTCCTCGGTATGAACATGCATGAAATTATACAGTGCTGAACCCAGGGAG
GTGCTTCCCACAGCCTCGAGGCCCTGTAGAGAAGTGGCCAACCTGATTGATGAGCCTTTGA
CCAAGGCAACTGTGCAGGCTCTGGGCCTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGACACATGACGCCGTGTCCGTGCCCCAGAACCTGCTGTCTTGAC
ACCCACCAGCAGCAGGGCTGCCCGGGCTCGATGGTGCTGGTGGTTCTGCGTCG
CCGAGGGGTGGTGTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGGCAAGCGCCAGGCCACTGCC
CACTGCCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACGCCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCACTCCTGGGGCC
CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGCACGGCGTCAATGAGTGCACATCGAG
AGCTCGTGTGGCGTCTGGGCCTGGGCGCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGCCCAATG
GGCGGTGACCCAGCCTCGCCGACAGAGCCGGGGCGCAGGCCGGCGCCAGGGCGCTAAT
CCCAGCGCGGGTCTCGCTGACCGAGCAGCCCGCTGGGAGCCGCGGGCAGGCAGACTGGCG
GAGCCCCCAGACCTCCCAGTGGGACGGGGCAGGGCTGGCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCCTCTGGCGCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATAACCCACCCAACTCCGTATTCTTTTTTTTTAGACAGGGTCTTGCTCCG
TTGCCCAAGGTTGGAGTGCAGTGGCCCACAGGCTCACTGTAACCTCCGACTCTGGTTCA
AGTACCCCTCCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCAACACCTGGC
TAATTTGTATTTGTAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTCGAACT
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCTCCAAAGTGCTGGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTCAAGATATTATTTCTTCACTGTTAAAA
TAAAACCAAAAGTATTGATAAAAAAAA

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCRRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG
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N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCCTTTCCACAGCAAGCTNTGCNATCCGATTGTTGCTCAAATCCA
ATTCTCTTGGGACACATNACGCCTGTCCTTNGCCCCAGAACCTGCTGTCTGTACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTTCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGGCAAGGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTATGGAGG
TGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTGGG
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTGGCCCTGCAGCCAGGCAGTGCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCATCCTT
GCGCTGCTCCCTGCACTCGGCCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAAGTGGGAGCCTGTCCTGGTCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCTGACCCCTCCATGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCCTAACCCCTGTGCTCAGGCACCTCTCCCCCAGGAAGCCTT
CCCTGCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTGTTGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

FIGURE 9

MTHRTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSDT
DPPADGPSNPLCCCFHGPATSTLNPLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCACCGCGTCCGAACCTCTCCAGCGAGGGAGCCGCCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGCGGAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTGTGGAGAACAACTATAACGCCCTCCAGAACGCCGGCACGAGG
GCTGGTTCATGGCCTTCACGCCGCAGGGGGCGCCAGGCTTCCGCAGCCGCCAGAAC
CAGCGCGAGGCCCACTTCATCAAGGCCCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAAGCAGAAGCAGTCAGTTGTGGCTCCGCCAACCGCCGGACCAAGCGCACAC
GGCGGCCAGCCCTCACGTAGTCTGGAGGCAGGGGCAGCAGCCCTGGCCGCTCCC
CACCCCTTCCCTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCCTGAGGGCCGGAAGCATCCGAGCCCCAGCTGGGAAGGGCAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTGCCCTCCGGACGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTACCCCTGATCTCAGGCCACCAGCCTGCGCCCTCCAGCCGGCTCTGAAGCC
CGCTGAAAGGTAGCGACTGAAGGCCTGCAGACAACCGTCTGGAGGTGGCTGCTCCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTAGCCCCAGCCCCAAACTCCTCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTGTTCAAGGAAAAAGAAAGGGAGAGAGAGGAAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCAACTCCCAGCCC
CGGAATAAAACCATTTCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPGSKDCVFTEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACCTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTCGCACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGACTTCACAGAACCCCATCCAGT
CATTTGATTTGCTGTTATTTTTTCTTTTCTTCCCACCAATTGTATTTAT
TTCCTGACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGCTTTTCCT
GAAGTCTGGCTTATCATTTCCCTGGGGCTACTCACAGGTGTCACAAACTCCTGGCCTGCC
CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAAACAAACAAATTAAATGCG
TGGATTTCCTGCAGAACTGCACAATGTACAGTCGGTGACACGGCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTCCAAGAATGTCAGAGTTCTCCATTGCAAGGAAAAC
AAATTCAAGACCATTACGGGCTGCTTGCCAGCTCTGAAAGCTGAAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGGCTTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAAATCGAATTGCTGTCATATCCGACATGGCCTCCAGAA
TCTCACGAGCTGGAGCGTCTTATTGGACGGAACCTCCTGACCAACAAAGGTATCGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCACCGTACGTCATTGCTGTCC
CACCCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACCAAGAT
AAACCACATTCTTGACAGCCTCTCAAATCTCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGTTTGATAATCTCTCCAAACCTGAAGCAGCTC
ACTGCTCGGAATAACCCCTGGTTTGACTGCACTATTAAATGGGTACAGAATGGCTCAA
ATATATCCCTTCATCTCTCACAGTGCGGGGTTCATGTCACAGGCTCTGAACAAGTCCGGG
GGATGGCGTCAGGGATTAAATATGAATCTTGTCTGCTCCACACGACCCCCGGCTG
CCTCTTCACCCCAGCCCCAAGTACAGCTCTCCGACCAACTCAGCCTCCACCCCTCTAT
TCCAAACCTAGCAGAAGCTACACGCCTCAAACCTTACACATCGAAACTTCCACGATT
CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTCTGAACGGATCCAGCTCTATC
CATTTGTGAATGATACTTCAAGTCAGCTGGCTCTCTCTTACCGTGATGGCATA
CAAACTCACATGGGTGAAATGGCCACAGTTAGTAGGGGCGATGTTAGGAGCGCAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
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CACCAACCATGCCTCTATCTGAACACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGGGCTGATCGGGGGCGCGGTGATATT
GTGCTGGTGTCTGCTCAGCGTCTTGCTGGCATATGCACAAAAAGGGCGCTACACCTC
CCAGAAGTGGAAATACAACCGGGCGCGGAAAGATGATTATGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCCTGGAGATGACAGAAACCAGTTTCAAGATCGTCTCCTTAAATAACGAT
CAAACCTTAAAGGAGATTCAGACTGCAGCCATTACACCCAAATGGGGCATTAAATT
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTGCAGACCTGGAGC
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCGACAATTAGACTCTTGAGAA
CACACTCGTGTGACATCAAAGACACGCGAGATTACATTGATAAATGTTACACAGATGCAT
TTGTCAGTTGAATACTCTGTAATTATACGGTGACTATATAATGGGATTAAAAAAAGTG
CTATCTTCTATTCAAGTTAATTACAAACAGTTGTAACCTTGTCTTTAAATCTT

FIGURE 13

MGLQTTKWPShGaffLKSLLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPaelHNVQSVHTVLYGNQLDEFPMLPKNVRVLHLQENNIQTI
SRAALAQLLKLEELHLDNSISTVGVEDGAFREAIISLKLFLSKNHLSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCS1KWKVTEWLKYIPSSLNVRGFMCQGPEQVRGMARVELNMNLLSCPTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTTSLPTIPDWDGRERVTTPPISERIQLSIHFVND
TSIQVSWLSSLFTVMAYKLTWVKGHSIVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLLV
LSVFCWHMHKKGRYTSQKWKYNRGRRKDDYCEAGTKKDNSILEMTETSQIVSLNNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGCGCGCGGAGACAGAGGCAGAGGCAGAAGCTGGGCTCCGTCCGCCTCCACGAGCG
ATCCCCGAGGGAGGCCGCGCCCTCGCGAGGCAGAGGAGGCCAGAGGAAGACCCGGGTGGCTGCGCCCTGCC
TCGCTTCCCAGGCAGCCGGCTGCAGCCTGCCCCCTCTGCTCGCCITGAAAATGGAAAAGATGCTCGCAGGCT
GCTTCTGCTGATCCTCGACAGATCGTCTCTCCCTGCCAGGGCAGGGAGCGGTACAGTGGGAGGTCCATCT
CTAGGGCAGACACCGCTCGAACCCACCCGAGACGGCCCTCTGGAGAGTCTCTGTGAGAACACAAGCAGG
TGGTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGGAGTTCATCGTGG
ACA TCTTGCATTCTGGACATTGGTCTGTGTCACCCGAGTGGGCTGCTCCAATATGGCAGCACTGTCAGAATG
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCGTGTCAAGAGGATGCCATCTGTCACCG
GCACCATGACTGGCTGGCATCCAGTATGCCCTGAACATCGCATTCTCAGAACAGGAGGGGGCCGGCCCTGA
GGGAGAATGTGCCACGGGTCAATAATGATCGTACAGATGGGAGACCTCAGGACTCCGTGGCCAGGGTGGCTG
AGGCACGGGACACGGGCATCCTAATCTTGCCATTGGTGTGGCCAGGTAGACTCAACACCTTGAAGTCCATTG
GGAGTGAGCCCCATGAGGACCATGTCTCCCTGTGGCAATTTCAGCCAGATTGAGACGCTGACCTCCGTG
AGAAGAAGTTGTGACGGCCACATGTGCAGCACCTGGAGCATAACTGTGCCACTCTGTCATCAACATCC
GCTCATACGTCGAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCAGAATCCAGGATCTG
GTGCCATGGAGGACCACAACGTGAGCAGCTGTGTGAATGTGCCGGCTCTCGCTGCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGGCTGACTACTGTGCCCTCAGAAAACCACGGATGTGAAC
ATGAGTGTGAAATGCTGATGGCTCTACCTTGCCAGTGCATGAAGGATTGCTCTTAACCCAGATGAAAAAA
CGTGCACAAGGATCAACTACTGTGCACTGAACAAACCGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGG
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGAAAACCTGCAGCCAGTGACACTGTG
AGCAGGACCATGGCTGTGAGCAGCTGTGTGAACACGGAGGATTCTCGCTGCCAGTGCTCAGAAGGCTTCC
TCATCAACGAGACCTCAAGACCTGCTCCGGGTGGATTACTGCCCTGCTGAGTGACCATGGTTGTGA
GTGTCACATGGACAGATCCTTGCCTGTCAGTGTCTGAGGGACACGTGCTCCGCAGCGATGGGAAGACGTG
CAAAATTGGACTCTTGTGCTGGGGACACCGTTGTGAACATTGTGTGAAGCAGTGAGATTGTTGTG
GCCAGTGCTTGAAGGTTATATACTCCGTGAAGATGGAAAACCTGCAGAAGGAAAGATGCTG
ACCATGGCTGTGAACACATTGTGAACAGTGACGACTCATACACGTGCGAGTGCTTGAGGGATCCGGCTG
CTGAGGATGGGAACGCTGCCAGAGGAAGGATGTCTGCACCATGGCTGCCAACACATTGTGTTA
ATAATTGGAAATTCCATCTGCAAATGTCAGAGGGATTGTTCTAGCTGAGGAGCGGAAGACGGTGC
GCACTGAAGGCCAATTGACCTGGCTTGTGATGGATCCAAGAGTCTTGGAGAAGAGAATTGAGGTC
TGAAGCAGTTGTCACTGGAATTATAGATTCTTGACAAATTCCCCAACGCGCTCGAGTGGGCTG
ATTCCACACAGGTCCACACAGAGTCACTCTGAGAAACTTCAACTCAGCCAAGACATGAAAAAAGCC
ACATGAAATACATGGGAAGGGCTATGACTGGCTGCCCTGAAACACATGTTGAGAGAAGTTTACCC
GAGAAGGGCCAGGCCCTTCCACAAGGGTGCCAGACGCACTGTTGAGGAGACATCTTACGGCTCAGGATG
ACGTCTCGAGTGGGCCAGTAAAGCCAAGGCCATGGTACACTATGTATGCTGTTGGGTAGGAAAAGCC
AGGAGGAACATACAAGAGATTGCTCTGAGGCCACAAACAAGCATCTTCTATGCCAGACTCAGC
ATAATGGAGATAAGTAAAAACTCAAGAAAGGATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGG
ACTCTCCAGGGGAACCTTGCAAAACGAAGAAGTAAGAAAATTAAACACAGCGCTTAGAAGAAATG
ACACAGAGAATGGCCAAACAGGATCAAGATTAAGATTAGAAAATCGCGAACACATTGTTAGTCATTG
TATCACGGATTACAATGAACCGCAGTGCAAGGCCAAAGCTCAGGCTATTGTTAAATCAATA
TGTGAGTAAAGTAACTAAGTATACTAAGTGTATAAAATTATCTAGGAAAAAAATCCT
TCAGAATTCTAACGATGAATTACCAAGGTGAGAATGAATAAGCTATGCAAGGTATTGTA
AACTTGCTTCTGCCTCATCCTGCCTTAGTGTGCAATCTCATTGACTATACGATAAAGTTGC
ACAGTCTTACTCTGAGAACACTGGCCATAGGAAATGCTGTTTTTGTA
CTGTAGAACACTGGCCATAGGAAATGCTGTTTTTGTA
CTGGACTTACCTTGATATACTGATA
TGTGATGATGATGATGATGATGATG
CATAAAATCATAGGACATATGTACTTGTG
GAACAAGTTGGATTTTTATA
CAACATATTAAACATTACCA
CTTCAG

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FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSGRSISRGRHARTHPOQALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV
KMRHLSTGTMGLAIQYALNIAFSEAE GARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAI GVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKG
EHECVNMEESYYCRCHRGYTLDPNGKTCRSVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRS DGKTCAKLDSCALGDHGCE
HSCVSSEDFVCQCFCFGYILREDGKTCCRKDVCQAI DHGCEHICVNSDDSYTCECLEGFR
LAEDGKRCRKRKVCKSTHHGCEHICVNNNSYICKCSEGFLAEDGRRCKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIDS LTISPKAARVGLLQY STQVHTEFTLRFNSAKDMK
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAK
GITMYAVGVGKAIEEEELQEIASEPTNHLFYAEDFSTMDEISEKLKKGICEALEDSDGRQDS
PAGELPKTVQQPTES EPTNINI QDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCGTCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCGGTTTTGTTCTGGGCTGA
CATGATTTCCCTCCCGGGCCCTGGTGACCAAATTGCTGCGGTTTTGTTCTGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGCCAGCTGCAACTGCACCTGCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTGCTCCAGCGTGGTACACCTTGACACGGGAGGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTGATGTGGTTCTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCTCGCGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGCAAATCTAGGGCCACAGCATAAAACCT
TAGAACTCAATGTACTGGTCTCCAGCTCCTCCATCTGCCGTCTCCAGGGTGTGCCCCAT
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCCTGTCCAATACCA
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGACCCAGCATTAGATGTCATCCGTG
GGTCTTAAGCCTCACCAACCTTCGTCTTCCATGGCTGGAGTCTATGTCAGGCCAC
AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTTGACTGGGACTGGGTTGCTGGCTGGCTGGTCC
TCTTGTACCACCGCCGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCTGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGACCC
TTCCTCTGTACCTCCGACGCCCTCCGCCACCCATGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGGCCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTAT**GATGAC**
CCCACCACTATTGGCTAAAGGATTGGGCTCTCCTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTC
TTTACTGTGGAAAACCCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGAGGAGCCTCACCCACCCCTGACTCCTCCTATGAAGGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTCCAGTCAGTGAGTCTCCAGGC
CCCCCTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTACTGGGGCAGAGGATAGGAAATCTC
TTATTAAAACATGAAATATGTGTTGTTCTATTGCAAATTAAATAAGATAACATAA
TGTGTTGATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQ
WDRQLPSFQTFFAPALD VIRGSLSLTNLSSSMAGVYVCKAHNEVGTACQCNVTLEVSTGPGAA
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

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FIGURE 18

CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCGCTCTAGTGGTTTTCCACTTT
TTGAATTGTTCTATACTCAAATTGACCAAGACACCTGCTTCCAAATGCAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGGAAATTAACTCAGTCTGGCGAAAATGCTAATTG
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTCAGATCCAGCAGTAACCA
AGACAGGTTTACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGCCATT
TAGATAATGTCGTATAGCTGCAAATATTAAATAAAAATTAACTTAAACAAAATCAGATCATAAAA
GAACCTGTGGCTTGCTACAAGAAGTCTAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATTAGCTGAATCATCTTCACTACTAGGTACAGAACAAACA
CTATCTCAGCCAAGGACACCCTTCTAACTCAACTCTTACTGAATTGTAACAAACCGTGAAT
AATTGTGTCAGGATACATTGTAGTTGGACAAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACATGCAACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTGAT
TCATATAACATGAAACATATTCTCATATGAATATGGATGGAGACTACATAAATATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTATTTATA
AGAGTATTGGCTTGTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAATTATGAT
AATTCTGAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCTAGTCAATGAGCTCAAACCC
ACCCACATTATATGAACATTGAAAAAAATAACATTACATTAAAGTCATCGAAAGGTACAGATA
GGTATAGGAGTCTATGCACTTGGATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATT
TTACAAGGATCACTCAACTAGGAATAATTATTCAGTATTGCTTGTGGCATATGCAATT
ACCTTCTGGTTCTTCAGTGAATTCAAAGCACCAGGACAACAATTCAACAAAATCTTGCTG
TAGCCTATTCTTGCTGAACCTGTTTCTTGTGGATCAATACAATAACTAATAAGCTCT
TCTGTCATCATTGCCGACTGCTACACTACTTCTTTAGCTGCTTGCATGGATGTGC
ATTGAAGGCATACATCTATCTCATGTTGTGGGTGTCATCTACAACAAGGGATTGGCA
CAAGAATTTTATATCTTGCTATCTAACGCCAGCCGGTAGTTGGATTTCGGCAGCAC
TAGGATACAGATATTATGGCACAAACCAAGTATGTTGGCTTAGCACCGAAAACAACCTTATT
TGGAGTTTATAGGACCAAGCATGCCATTCTGTTAATCTCTGGCTTGGAGTCAT
CATATACAAAGTTTCGTACACTGCAGGGTTGAAACCAAGCAGTTAGTTGCTTGGAGAAC
TAAGGTCTTGTGCAAGAGGAGCCCTCGCTCTGTGTTCTCGGCACCACTGGATCTT
GGGTTCTCCATGTTGTGCACGCATCAGTGGTACAGCTTACCTCTTCACAGTCAGCAATGC
TTTCCAGGGATGTTCATTTTATTCTGTGTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTCAAAAATGTCCTGTTGTTGGATGTTAAAGGTAACATAGAGAATG
GTGGATAATTACAACACTGCACAAAAAATTTCAAGCTGTGGATGACCAATGTATAAAA
TGACTCATCAAATTATCAATTAAACTACTAGACAAAAAGTATTAAATCAGTTTCT
GTTTATGCTATAGGAACGTAGATAATAAGGAAAATTATGTATCATATAAGATATACTATGT
TTTCTATGTGAAATAGTCTGCAAAATAGTATTGAGATATTGGAAAGTAATTGGTTT
CTCAGGAGTGTATCACTGCACCAAGGAAAGATTCTTCTAACACGAGAAGTATATGAA
TGTCTGAAGGAAACCACTGGCTTGATATTCTGTGACTCGTGTGCTTGAACACTAGTCC
CCTACCACCTCGGTAAATGAGCTCCATTACAGAAAGTGGACACATAAGAGAATGAAGGGCAGA
ATATCAAACAGTGAAGGAAATGATAAGATGTATTGAAATGAACCTGTTCTGAAACTAGTCC
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAGAACACATTACCACTTTGTGAA
TTGTTCTGAACCTAAATGTCCACTAAACAACTTAGACTCTGTTGCTAAATCTGTTCTT
TTCTAATATTCTAAAAAAAGGTTACCTCCACAAATTGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENVANCHLDNVCIAA
NINKTLTKIRSIKEPVALLQEYVRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL
SNSTLTFVKTVNNFVQRDTFVVWDKLSVNHRRTLTKLMHTVEQATLRIQSFKTTEFDT
NSTDIALKVFVFFFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSGNVAVAFLYYKSIGPLLS
SSDNFLLPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDYRSLCAF
WNYSPDTMNGWSSEGCELTYSNETHTSCRNCNLTHFAILMSSGPSIGIKDYNILTRITQLG
IIISLICLAI CIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFC SIIAGL
LHYFFLAAFAWM CIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSAA LGYRYYGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVVLHVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAAATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT
TGGTCCTTGCTTCATCATCTGACAACCTCTTATTGAAACCTAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTCACTGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAAGGTATA
GGAGTCTATGTGGCATTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTTGTCTGCCATATGCATTTTACCTTC
TGGTTCTTCAGTGAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCC
CTAAGCGAGGCCTCCTCCCTCCCAGATCCGAACGGCCTGGCGGGGTCAACCCGGCTGGGA
CAAGAAGCCGCCGCTGCCCTGCCCGGGGGAGGGGGCTGGGCTGGGCTGGGCCGAGGCGG
GGTGTGAGTGGGTGTGCGGGGGCGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGTCTGGCACCTACCGTGGGGCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG
CCGCCGCCGCGTCAGAGCAGGAGCGCTCGCTCAGGATCTAGGGCACGACCATCCAAACCC
GGCACTCACAGCCCCGAGCGATCCCGTCGCCGCCAGCCTCCGCACCCCCATCGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCGGCCCTCGCCTTCTCGGACGCCGGGCC
CCACGTGCACTACGGCTGGGGGAGACCCATCCGCCTGCCGACCTGTACACCTCCGGCCCC
ACGGGCTCTCCAGCTGCTCCTGCGCATCCGTGCCGACGGCGTGTGGACTGCGCCGGGG
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTCGGACCGTGGCATCAAGGG
CGTGCACAGCGTGCGGTACCTCTGCATGGCGCCAGGCAAGATGCAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAAGCACGCCCTCCGGTCTCCCTGAGCAGTGCAAACAGCGGAGCTGTACAAGAA
CAGAGGCTTCTCCACTCTCTCATTCCTGCCATGCTGCCATGGTCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGGAAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTGGGCTTGTCAACCGGACTGGAGGCCGTGAGGAGTCCAGTGTGAGAAGTAAC
GAGACCATGCCGGCCTCTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGACG
TGCTTCTACAAGAACAGTCCTGAGTCCACGTTCTGTTAGCTTAAAGGAAAGAACATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCCAGTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCCTGGGCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGAAC
TCACTCCTTGGAAAATTCTATGTCAAGCTGAAATTCTCTAAATTCTCATCCTGCA
CCCAGGAGCAGCCAGAACAGACAGGCAGTAGTTAATTCAAGGAAACAGGTGATCCACTCTGTA
AAACAGCAGGTAAATTCACTCAACCCATGTGGAAATTGATCTATATCTACTTCCAGGG
ACCATTGCCCTCCAAATCCCTCCAGGCCAGAACACTGACTGGAGCAGGCATGGCCCACCAAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGGCCCTGGGACAACGTGAGAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGCTGCCAGAATAACTTGCTGTCCCGGTGTCACCTGC
TTCCATCTCCCAGGCCACCGGCCACTCAGCTGCCACCTCACATGCCTCCCATGGATTGGGGCCT
CCCAGGCCCTCCACCTTATGTCAACCTGCACTTCTGTTCAAAATCAGGAAAGAAAAGAT
TTGAAGACCCCAAGTCTGTCAATAACTTGCTGTGGAAGCAGCGGGGAAGACCTAGAAC
CCTTCCCCAGCACTGGTTTCCAACATGATATTATGAGTAATTATTATGTATGTAAAGTGAGGTTG
TCTCTTATTCTTACATTATTATGCCCAAAATTATATTATGTATGTAAAGTGAGGTTG
TTTGATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHLRPLVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTCAAGGGCCCCGGCCTCCTGCCTGCCTGCCGCCGGACCCCTGACCTCCTCA
GAGCAGCCGGCTGCCGCCGGAAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTGCTG
CTGCTGCCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCAA
AGAAGACTGTTCCAGATTAGAGTGGAGAAACTGGGTGGAGTGTCTCCTTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAATGTGACAAGAAGTGTGATGCCGGAAATATCGTTGTGAAGTTAGTGCCTCATCTG
AGCAAGGCCAAACCTGGAAGAGGATACAGTCAGTCTGGAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGAATCCAGCTCCTGAATAACACATGGTTAAGGATGGCATCCGTTGCTAGAAA
ATCCCAGACTTGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAAACTGGAAC
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCCCTGTGAAGCCCGCAATT
TGTTGGATATCGCAGGTGTCCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCGTAGTAGTTGTGGCCTAGTGATTTCCGTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTGGAAATGTGCAGTGGCTCACGCCGTAACTCCAGCACTTGGAGG
CCGGCGGGCGGATCACGAGGTAGGAGTTCTAGACCAACTGGCCAATATGGTGAACCC
CATCTCTACTAAAATACAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTGAACCCGGAGGCGGAGGTTGCAGTGAGCTGAGATCACCG
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAATAAAATAAAATA
AATAAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDDQQVVTAVEYQEAILACKTPKKT
VSSRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQ
GQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD
GIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN
SVGYRRCPGKRMQVDDLNISGIIAAVVVVA
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPV
IPALWKAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTAAACATGCTCACAGCCGGACCCCTGGCAT
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGGATTAAATATTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTACATACTCCACCTTCAAAAAGTACATCAATA
TTATATCATTAGGAAATAGTAACCTCTCTCCAAATATGCATGACATTGGACAATG
CAATTGTGGCACTGGCACTTATTCAGTGAAGAAAAACTTGTGGTTATGGCATTATCA
TTTGACAAATGCAAGCATCTCCTTATCAATCAGCTCTATTGAACTTACTAGCACTGACTG
TCCAATCCTAAGGGCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCTATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTTCCCAGCCAGATTGCC
AGCTAACACACAGATTCTCCTACAGACTAACATATTGCAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTACTGGCCTGGATTATCTCAAAACAAATTATCAGTCACCAAT
ATTAATGTAAGGAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAACAAACTTACTGA
ACTGCCTGAAAATGCTGTCCGAACGTGAGCAACTTACAAGAACTCTATATTAAATCACAACT
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTTCTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT
TCTGATGATTGGGAAAATCCAATTATCAGAACAGACATGAACTTTAACGCTCTTATCA
ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCCTGGTT
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCCATGT
TGCTCTCAAAAGTTGTAATCTCAAATTGGATCTAAATAAAATCCTATTAAATAGAA
TACGAAGGGGTGATTAGCAATATGCTACACTAAAGAGTTGGGATAAAATAATATGCCT
GAGCTGATTCCATCGATAGTCTGCTGGATAACCTGCCAGATTAAAGAAAATAGAAC
TACTAACACCCCTAGATTGTCTTACATTCCCCAATGCATTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCTGGTACTCTG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTACTGTGATCCGTG
GATGAACATGAACAAAACCAACATTGATTGAGCCAGATTCACTGTTTGCCTGGACC
CACCTGAATTCCAAGGTCAAGATGTTGGCAAGTGCATTTCAGGGACATGATGGAAATTG
CTCCCTCTTATAGCTCCTGAGAGCTTCCTCTAAATCTAAATGAGAAGCTGGAGCTATGT
TTCCTTCAGTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTCTG
GTCAAAACTCTGCCTAATACCCGTACAGACAAGTTCTATGTCCTATTGAGGGAAACACTA
GATATAATGGCGTAACTCCCAAAGAAGGGGTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTGAAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAAATG
GCTCTTGAATATTAAAATAAGAGATATTCAAGGCCAATTCAAGTTGGTGTCTGGAAAGCA
AGTTCTAAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA
TGCTGCGCAAAGTGCCTGAATACCATCTGATGTCAGGTATATAATCTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTACAGAAAAACAGAAAAAAA
TGTGAAATGTCACCACCAAGGTTGCACCCCTGATCAAAAAGAGTATGAAAAGAATAATAC
CACAAACACTTATGGCCTGTCTGGAGGCCTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCCAGAAATGAACGTGATGGGGACACAGCTATGTGAGGAATTACTTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGTATAAATCTCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCT
AAAAACCACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMLPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNIAKIEYSTDFPVNLTLQDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELNLQELYINHNLSTISPGAFIGLHNLRLHLNSNRQLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRLSIVAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVNLKFLLDKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSALYHTGIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEPDSSLFCVDPPFEFGQGQNRQVHFRDMMEICLPLIAPESFPSNLN
EAGSYVSFHCRATAEPQPEIYWIITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARI PSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLGIIGVICLISCLSPEMNCDGGSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSLKVATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583, 608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site

amino acids 570-579

N-myristoylation site

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence

amino acids 277-280

FIGURE 27

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGTGGAGTAGATGAGGAATGGCTCGTATTATGCTGACATTCCAGC**ATGAATCT**
GGTAGACCTGTGGTTAACCGTTCCCTCCATGTGTCTCCTCCTACAAAGTTTGTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTGTCTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTCAAAGGAGTAGCTGAAACCTTGAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAATGCCTCAATAACCTGAAGGCCAGGCCAGAATTGCCAACACCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTGGCTGGTTCACTATGGTGTCTCATATGTGGTATTATGTGAGGCAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGT**ATAGTGT**CCAAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTGCATTGCAGTAGAAATAAGTGGTTACTTCTCCATCCATTGTAAACATTTGAA
ACTTGTATTCAGTTTTTGAAATTATGCCACTGCTGAACCTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAATAATGAAATTATTTTTT
AATTAAAAGCAAATAAAAGCTTAACTTGAACCAGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLCSSGGLNVTCSNANLKEIPRDL
PPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSLDR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPF
LNAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristylation site.

amino acids 37-43, 45-51, 110-116

4960620 0202006600

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCGAG**TG**CAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCACCTCCTGCTGGTGCT
GGGCTCAGTGTGTCAGGCTCGGCCACGGCTGCCGCCCCGCTGCGAGTGCTCCGCCAGG
ACCGCGCTGTGCTGCCACCGCAAGTGCTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTTCGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCTGGAGGCCGGCG
CCTTCAACAACCTCTCAACCTCCGGACGCTGGGTCTCCGCAGCAACGCCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCAGAACAAGAT
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCACCGCCTCAGCGGCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCTGTCCCACCTGCACGGCCT
CATCGTCTGGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCTACTTGGACACCATGACACCCAAC
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCCCTCAACCTCTCCTACAAACCCATCA
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGCG
GGGAGCTGCCGTGGTGGAGGCCCTATGCCTTCCGGCCTCAACTACCTGCGCGTGTCAA
TGTCTCTGGCAACCAGCTGACCAACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG
AGACACTCATCCTGGACTCCAACCCGCTGGCTGCAGCTGCGCTCCTGTGGTGTCCGG
CGCCGCTGGGGCTCAACTCAACCGCAGCAGCCCACGTGCGGCCACGCCAGGTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTCACCTGCCGCCGG
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTGGACGAGGGCACACGGTCAGTT
GTGTGCCGGGCCATGGCGACCCGCCGCCCCCATCCTCTGGCTCTCACCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGGGCTCACAGTCTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGGGGGGCAACGAC
TCCATGCCGCCACCTGCATGTGCAGCTACTGCCGACTGGCCCCATCAGCCAACAA
GACCTCGCTTCATCTCAACCAGCCGGGAGGGAGAGGCCAACAGCACCCGCCACTG
TGCCTTCCCTTCGACATCAAGACCCTCATCATGCCACCACATGGCTTCTCATCTTT
CTGGCGTGTCTCTTCTGCTGGTGTGCTGTTCTCTGGAGCCGGGCAAGGGCAACAC
AAAGCACAACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAGGCATCAGCTCCGCC
ACGCCGCCAGTTCAACATGAAGATGATA**TG**AGGGCGGGGGGGGGCAGGGACCCCG
GGCGGCCGGGCAGGGGAAGGGGCCTGGTCGCCACCTGCTCACTCTCCAGTCTTCCACCTC
CTCCCTACCCCTCTACACACGTTCTCTTCTCCCTCCGCCCTCGTCCCTGCTGCCCG
CCAGCCCTCACCACTGCCCTTCTACCGACCTCAGAAGCCCAGACCTGGGGACCCCA
CCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTC
ATAATTCAATAAAAAGTTACGAACCTTCTGTAACTTGGGTTCAATAATTATGGATTT
TATGAAAATTGAAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPIIILVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL
GLRSNRLKLIPLGVFTGLSNLTQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTLEESVFHSVGNLETLILDSNPLA
CDCRLLWVFRRRWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPIALWLSPRKHLVSAKSNGRLTVFPDGTLEVRYAQVQDNGTYL
CIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCACGCGTCCGACCTCGGCCCCGGCTCCGAAGCGGCTCGGGGGGCCCTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGCGCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGCCCCAGCCGCTCGCTCTGCTCCTGCTCCTGC
TGTCGCCTGCTGCTGGCGCCGGGGCAACCTCTCCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGTCAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGCTAACCTGCTCAGCAGACTCTACTTGGGAGAAGA
GAGCCCTCGAGATAATCGAATTCACTGGTACCTCTACGCCAACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAAGCCCATCATCACTGGTT
ATAAAATCTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTCTGGGAGCAAG
CCTGCAGCCCCGGCTCACCTGGAGAAAGGGTACCAAGAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCCAATGGTAAAACCTCACTGTCAGCAGCTCGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTCCTCAACAAGAGTGAAGTGGCACCTACGGCTGCACAGCCACCA
AACATGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT
CCTCCTCCAGCACCTACCACGCCATCATCGTGGGATCGTGGCTTCATTGTCTCCTGCTG
CTCATCATGCTCATCTTCCCTGGCCACTACTTGATCCGGACAAAGGAACCTACCTGACACA
TGAGGCAAAGGCTCCGACGATGCTCCAGACGCGGACACGCCATCATCAATGCAGAAGGGC
GGCAGTCAGGAGGGACGACAAGAAGGAATATTCATTAGAGGGCGCTGCCACTTCTGC
GCCCCCCAGGGGCCCTGTGGGACTGCTGGGGCGTCACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAAATGTCTGC
TTTGGGTGCGGTTTGACTCGGTTGGAATGGGAGGGAGGAGGGCGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGGTTATTATTATTGGTAACAATCC
CAAATCAAATCTGTCCTCAGGCTGGAGAGGCAGGAGGCCCTGGGGTGAGAAAAGCAAAAAACA
AACAAAAAACA

FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRQLVTSTPHELYSISISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

TOEITZ0-02260660

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTCTCCTTCTGG
CTTCGGACATTGGGACACTAAATGAACCTGAAATTGTGCTGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTGCTTAAATGCTGCTTGGATTCTGTT
GCTGGAGACGTCTCTTGTGCTGGAAACGTTACAGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCAGTTACCAATTATTCATGGCAATT
CCTCACTCGACTTTCCCTAATGAGTCGCTAACCTTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTTGCATGAAATCGTCCGGGGCTTTCTGGGCTGCAGCTGGTAAAAGG
CTGCACATCAACAACAACAAGATCAAGTCTTTCGAAAGCAGACTTTCTGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAAGACCCGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTAAATGACAATCTCATCAGCACCCACTGCCAAC
GTGTTCCAGTATGTGCCCATACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCC
GGGACTGCACCTGTGATCTGCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGCTTGTGAAAACCGAGTGGATTCTAGTCTCCGGGCCCGCTG
CCCAAGAAGAGACCTTGCTCCTGGACCCCTGCCACTCCTTAAGACAAATGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC
GTTTACCCCTGCCCTGGGGCTGCAGCTGCGACCACATCCCAGGGTCGGGTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTGGCTGATTTGAAGCCAAGCTCTAACGTGCAGGA
GCTTTCTACGAGATAACAAAGATCCACAGCATCCGAAAATCGACTTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTCAAG
AACCTTTGGACCTCAGGTGGCTATACATGGTAGCAATTACCTGGACACGCTGTCCGGGA
GAAATTGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAAACACTG
CTGAGGTCCCTGCCTGTGGACGTGTTGCTGGCTCTCGCTCTAAACTCAGCCTGCACAA
CAATTACTCATGTACCTCCGGTGGCAGGGTGCTGGACCAGTTAACCTCCATCATCCAGA
TAGACCTCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTCAACAGTGGGCA
GAACGCTTGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTT
TAGAAAGGATTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTAACCGCACAGTAAAACAGCACTGGGTTGGCGAGACCGGACGCACCTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTGGTGTGGCTCCGGACTGCTGCTGGT
GTTTGTACCTCCGCCTCACCGTGGGGCATGCTGTTATCCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACTCCTCCGCTCGAGATTAACTCCCTACAGACAGTCTGT
GACTCTCCTACTGGACAATGGCCTTACAACGCAGATGGGCCACAGAGTGTATGACTG
TGGCTCTACTCGCTCTCAGACTAAAGACCCCAACCCCAATAGGGAGGGCAGAGGGAGGG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCGCG
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTCGCACAAACGAAAGGGCT
GACCCCTACTTAGCTCCCTCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTTTGCTGAGAGGCCCTTTGACAGAAAGGCCAGCACGACCCCTGCTGGAAG
AACTGACAGTGCCCTGCCCTCGGCCCCGGGCTGTGGGTTGGATGCCCGGTTCTATAC
ATATATACATATCCACATCTATATAGAGAGATAGATATCTATTTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACCTTGACTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGDCVCKEKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPG AFLGLQLVKRLHINNNNIKSFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAFQDLNKLEVILLNDNLISTLPANVFQYVPI THLDLRG
NRLKTL PYEEVLEQI PGIAEILLEDNPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDILNETTEQDLCPLKNRVDSSL PAPPAQEETFAPGPLPTPKTNGQEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSDHIPGSGLKMNCCNRNVSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLLDGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNALQLILPGTFNAMPKLRILILNNNLLRSLPVDFAGVSL
SKLSLHN NYFM YLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEV LMSDLKC
ETPVNFFRKDFM LLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLL VFVTS AFTVV GMLV FILRN RKR SKR RDANSSASEINS LQTV CDSSYWHNG PYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGCACACATTCTCTGTCGGCCTAAGGGAAACTGTTGGC
CGCTGGGCCCGGGGGATTCTTGGCAGTTGGGGGTCGTCGGAGCGAGGGCGGAGGGGG
AAGGGAGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCCTCAGACAC
AGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCAGGGCCTCAG
AGAATGAGGCCGGCGTTGCCCTGTGCCCTCTGGCAGGCCTGCTCTGGCCCGGGCCGG
CGGCGAACACCCCACTGCCGACCGTGCTGGCTCGGCCCTGGGGCCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGCCGAGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCCCGAGCTGCCGCTGTGCTCGCCTCTGCGGGCAGGCCAGG
GCCCGGAGGGGGCTCCAAAGACCTGCTGTTCTGGGTCGACTGGAGCGCAGGCCTCCC
GCACCTGGAGAACGAGCCTTGGGGGTTCTCTGGCTGTCCGACCCGGCGGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGGCCAACGCTCTGCAACCGCGGGAGATGCGC
GGTACTCCAGGCCACCGGTGGGGTCGAGCCCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAAGTTGAGGTCTTGTGTCCTGCGCCGCCGG
GCCGCCTCTAACTTGAGCTATCGCGGCCCTCCAGCTGCACAGCGCCCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCCGATCTCAGTTACTGCA
TCGCGGACGAAATCGCGCTCGCTGGGACAAACTCTCGGGCGATGTGTTGTGTCCTGCC
GGGAGGTACCTCGTGGCAAATGCCAGAGCTCCCTAAGCTGCTAGACGACTGGGAGG
CTTGCCTGCGAATGTGCTACGGGCTCGAGCTGGGAAGGACGCCGCTTGTGACCA
GTGGGAAGGACAGCCACCCCTGGGGGACCGGGGTGCCACCAGGCCGCCGGCCACT
GCAACCAGCCCCGTGCCAGAGAACATGGCAATCAGGGTCGACGAGAACGACTGGGAGAGAC
ACCACTGTCCTGAAACAAGACAATTCAAGTAACATCTATTCTGAGATTCTCGATGGGGAT
CACAGAGCACGATGTCTACCCCTCAAATGTCCTCAAGCCAGTCAGGCCACTATCACC
CCATCAGGGAGCGTGATTCCAAGTTAATTCTACGACTTCTGCCACTCTCAGGCTTT
CGACTCCTCCTGCGGTCTTCATATTGTGAGCACAGCAGTAGTAGTGTGTTGATCT
TGACCATGACAGTACTGGGCTGTCAAGCTCTGCTTACGAAAGCCCTCTCCAGCCA
AGGAAGGAGTCTATGGCCCGCCGGCCTGGAGAGTGTACCTGAGCCGCTGCTTGGGCTC
CAGTTCTGCACATTGCAACAAACATGGGTGAAAGTCGGGACTGTGATCTGCGGACAGAG
CAGAGGGTGCCTGCTGGCGAGTCCCTCTGGCTCTAGTGTGCAAGGGAAACAGGGGA
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTAC
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATGAGAGAACGAGTGGAAAGTGCCTTAGGA
TGGTGTGAACTGGGGACGGTAGTGTGCTGGGAGAGATATTCTTATGTTATTGGAGAA
TTTGGAGAAGTGTGAACTTTCAAGACATTGAAACAAATAGAACACAATATAATTACAA
TTAAAAAAATAATTCTACCAAAATGAAAGGAAATGTTCTATGTTGTTAGGCTAGGAGTAT
ATTGGTTGAAATCCCAGGGAAAAAAATAAAATAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGP GGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVT S IPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVFIFVSTAVVVLVILTMVGLVKLCFHESPSSQPR
KESMGPPGLES DPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

70087400-02260650

FIGURE 37

CGGACGCGTGGATT CAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATAATCGCTTAAAAGTCGCTCCGCCCTGCCGGCGTAC
CCCCGGCTACCTGGGCCGCCCCGCGCGGTGCGCGCGT GAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGGTGTGAGGCCGGTGGGTGCGGA
GGGGCGTGTGTGCCGGCGCGCGCCGTGGGTGCAAACCCCGAGCGTACGCTGCCATGA
GGGGCGCGAACGCCCTGGCGCCACTCTGCCTGCTGGCTGCCGCCACCCAGCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCCCTGGAGTGTACCCCTCAAATAGCAAATGTACTTGAAAATCA
CAGTTCCCAGGAAAAGTAGTCGTTCAATTCCGATTCAAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTGTGGATGTGTACAATGCCATGCCAATGCCAGCGCATTGGCCG
CTTCTGTGGCACTTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGGCCATGTTCTCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTCCGGCTTTAAAAC
CCCCAAGTGGCCAGACCGGGATTACCCCTGCAGGAGTCATTGTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTTATTCACT
TTTATCAGACTTAAGTTAAGTGCAGATGGTTATTGGTCACTACATATTCAAGGCCAAA
AAACTGCCTACAACACTACAGAACAGCCTGTCACCACCATCCCTGTAACCACGGTTAAA
ACCCACCGTGGCCTGTGTCAACAAAAGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGAATTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCAGGGAGTTG
CACGCCACAGTCTGATCATCAACATCTACAAAGAGGGAAATTGGCGATTCAAGCAGGCAGG
CAAGAACATGAGTGCAGGCTGACTGTCGTGCAAGCAGTGCCTCTCCTCAGAAGAGGTC
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGCAGGAAATCATGCCAACAGC
TTTATCATGATGTTCAAGACCAAGAACATCAGAAGCTCCTGGATGCCCTAAAAAATAAGCAATG
TTAACAGTGAACTGTCCATTAAAGCTGTATTGCCATTGCCCTTGAAAGATCTATGTT
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAAGTTCT
TGCCCTGCTGTCAGAGGAGCAGCTATGATTGAAACCTGCCGACTTAGTGCAGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTGGAAAGCGTTATTATACATCTGTAAAAGGAT
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAAGATTTAGAAGTGCATATTATAGT
GTTATTGTTCACCTCAAGCCTTGCCTGAGGTGTACAATCTGTCTTGCCTTCTA
AATCAATGCTTAATAAAATTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTITRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

FIGURE 40

MAPWPKGLVPAVLWGLSLFLNLPGPWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCGPAGTFGPSCLPAGTERPCGGYGCQCEGEGTRGGSGHCDCQAG
YGGECAGQCGLGYFEAERNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIFKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

TO 87P20-02260660

FIGURE 41

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGACTCTGGGTGTTGCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTCAGCTAAAGAGGT
GCCCACCTGGACAGGGCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTCAAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTCGG
CATGGAGCAGCGCTGCCGCCAACAGCGAGCTGGTCAGGCCGTGCTGCCCTTCCAGG
AGCCGGTCCCCAAGGCCGCGTGCACAGGCACGGCGGCTGTCCCCGCCAGCGCCGGGCC
CGGGTGACCGTCGAGTGGCTGCGCGTCCCGCAGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGGC
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGCCGAGAACTGGGTGCTGGAGCCCCGGCTT
CCTGGCTTATGAGTGTGTGGCACCTGCCGGCAGCCCCCGGAGGCCCTGGCCTCAAGTGGC
CGTTCTGGGCCTCGACAGTGCATGCCCTGGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCTGCCAGGCCATAGGCGCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGGTGCAGGGTACCAAGGAGAGCTG
GCGATGACTGAAGTGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTTGCTCTCAGGAATGAGAATCTTGGCCACTGGA
GAGCCCTGCTCAGTTCTATTCTATTACTGCACTATATTCTAACGACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCATTGTTACTTGTCCGTAC
TGGATCTGGCTAAAGTCCACCACCACTCTGGACCTAACGACCTGGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTTGTAAAACATGAATAAACACATTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEHQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

T08T20-D2E606160

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGCGGGCTGTTGTCAGTGGCCTGATCGCGATGGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTCCTCTCATATTGGCGATCCTGTTGCTCCCTGG
CATTGGCAGTGTACAGTGCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCCGTGCCTACTCGGGCTTTCTCTCCCGTGGAGTGGAGTTGACCA
AGGAGACACCACCACTCGTTGCTATAAAACAAGATCACAGCTTCTATGAGGACCGGG
TGACCTTCTTGCCAACTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTCTGAATACACCTGGTCAAAGAT
GGGATAGTGTGCCTACGAATCCAAAAGCACCCGTGCCTCAGCAACTCTTCTATGTCC
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAAATGGGTATGGGACACCCATGACTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCTGAAGTGAAGGAGAACAAACAG
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTACCGCCTATCATCTGCATTGCCCTACT
CAGGTGCTACCGGACTCTGGCCCTGATGTCAGTTCACAGGATGCCTTATTGTCTTC
TACACCCCACAGGGCCCCCTACTTCTGGATGTGTTAATAATGTCAGCTATGCC
ATCCTCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACCTGTTAAA
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGCGGGGTCGCAAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTCTGGCTCTTCTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTGTCCTCCATGGGAAGTG
CCACTGGATCCCTCTGCCCTGTCCTCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAATGGAGCTTGTGGAGAGCATAGTAAATTTCAGAGAACTGAAGCCAAAAG
GATTAAAACCGCTGCTCTAAAGAAAAGAAAATGGAGGCTGGCGCAGTGGCTACGCC
TAATCCCAGAGGCTGAGGCAGGCCATCACCTGAGGTGGAGTCAGGATCAGCCTGACCA
ACATGGAGAAACCCACTGGAAATACAAGTTAGCCAGGCATGGTGGTGCATGCC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPEENNPKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELEVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

TOGETHER - 02260660

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCGCTTCCACCCGACCTCTGCCCAGGCCAGGCCAGCTCAG
GCTCGTGCCACCCACCAAGTTCCAGTGCCGACCACTGGCTTATGCGTGCCCCCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTCGGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCAACTGCCTATGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCCTCCTCTTGTCCCTGGCTCCGAGCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAACAGAC
CTCGCTGCCCTGAGGACAAGCACTTGGCACCACCGTCACTCAGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGACACCCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCDRDLCSDGSDEEECRIEPCTQKGQC PPPGLPCPCTGVSDCSGGTDKKL
RNCSRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCACCGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGAGCAGAGGTCGCGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGAGGAGGAAGGAAGGAGTGCATGCATGAGACCCACAGA
CTCTTGCAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
CGATGACCTCAAGTGTGTGCTGACCCCGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTCTTGAGGCTCTGTAGCCGATTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCTAGGCTGGATCCAAGTGA
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCAATTATGTCGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTCCCGTGGGACTGTGATCTCCTATCGCTGCTTCCCGATTAAACTT
GATGGGTCTCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTCTGTCT
GCCACCCCGCCCTTGTGAGCGCTACAACCACCGAACTGTGGTGGAGTTTACTGCGATCCT
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAGTGTGCTGCTGGTGTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCTCCCCGGAG
TTCCAGCAGTGACCTGACTTGTGGTGGTAGACGGCGTGCCTCATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTAGGCCCGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCTTACCCGTGGACGACCAGAGCCCCCAGCATAACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTGAGCTGCTCCAAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCACCCAGGATCCATGCCACTGGGT
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCAGGATCCATGCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTAAAAAATTCCAAAGTGCCTGAAGTGTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCCCTTCTCTTGGTTTAGACAAATGAAACAA
AGCTCTGATCCTAAAATTGCTATGCTGATAGAGTGGTGGAGGGCTGGAAGCTTGATCAAGTC
CTGTTCTTCTTGACACAGACTGATTAAAATTAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKGATKRLCLKHNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPPLVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCACCGCGTCCGCTCCGCGCCCTCCCCCGCTCCCGTGCCTGCAGCTCCACCGCCGT
TGCTGCTGCCCGGGTTGCAGTTGTCGCACGCCCTGCCGCCAGCCGCTCCACCGCCGT
AGCGCCCGAGTGCGGGGGCGCACCCGAGTCGGCCATGAGGCCGGAAACCGCGCTACAGG
CCGTGCTGCCGTGCTGGCTGGTGGGGCTGCCGCCAGGGCTGCCCTGCTGAGTGCC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTGTTA
TAAAGTCATTACTTCATGATACTTCTGAAGACTGAACCTTGAGGAAGCAAAGAACCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTCATTGAAAACCTCTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT
CACAATTAGGAACTGGTATGTGGATGAGCCGCTGCCAGGAGGTCTGCGTGGTATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACATTCATTGCAAATATTCTGATGAGAAACCAGCAGTCCT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAACATTAAAGAAAGTAGAGAACGCTGCCCTGAATCTGCCCTACAT
CCTAATCCCCAGCATTCCCCTCTCCTCCTGTGGTACACAGTTGTATGTTGGTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTAGCACAAAGAACACACCATC
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGCCAGACCTGAAGAATATTCTTCAGTGTGTT
CGGGAGAAGCCACTCCGATGACATGTCTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACCAAATGGGAGGAGTAAGGAGTCTGGATGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAACTGAAACTGACAACATGGAAAAGAAATGATAAGCAAATC
CTCTTATTTCTATAAGGAAAATACACAGAACGGTCTATGAACAAAGCTTAGATCAGGTCTGT
GGATGAGCATGTGGTCCCCACGACCTCTGGACCCCCACGTTGGCTGTATCCTTAT
CCCAGCCAGTCATCCAGCTGACCTTATGAGAACGGTACCTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCACTGGTTGGTTGTATCTAACCTTAAGGGACAGAGCTTACCTG
GCAGTGATAAAAGATGGCTGTGGAGCTGGAAAACCACCTCTGTTCCCTGCTCTACAG
CAGCACATATTATCATAACAGACAGAAAATCCAGAACATCTTCAAAGCCCACATATGGTAGCACAG
GTTGCCCTGTGCATGGCAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGQTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKKTFKESREAALNAYILIPSIPLLLLLV
VTTVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSEGFTLVSVESGFVTNDIYEFSQDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCGCTGAGCCCCGGCGCCCGAGAAGACTTGT
GTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCAATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCCAGTGGCGTCTGACCTCGTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTGACACGGGGCTGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTGGGAGAGAGACTGAGGAAGAACTATGTGGAAAGACATTCCCTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTAGAAGTCTTGTATCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGTAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCAAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGACTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG
TGACCTTCATACCGCTTTAATGACCCCTGGGATTTTGACCACAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACCAACGGGAAGGAGCAGGTGCCAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT
TTAAAATAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHLNPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCP LD MFLNAMS VY TLSPEKYHALCSQTQVM EVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTTGCAGCTAAACTAAATATTGCTGCTGGGGACCTCCTCTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTGCAACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGC~~GG~~CTGGTGGGGCCT
CCACCGCTGTGAAGGGCGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAACAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCCA
GTCCCAGAGGGTGTCA~~GG~~CTGGCTGACGGCCCTGGCATTGCAAGGGACGCGTGGAGTGAA
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAACGCTGCAACAAAGCATGCC
TATGGCCGAAAACCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTCA
GGATTGCCCTCTGGCCTTGGGAAAGAACACACTGCAACCATGATGAAGACACGTGGTCG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTCTGTGATGACAACACTGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGCTGTGGAGTCCCTCTCCCTCAGAGACCGGA
AATGCTATGCCCTGGGTTGCCGATCTGGCTGGATAATGTCGTTGCTCAGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTGGGTTTCAGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGACTTAACTTGGTGCCTGATTCTCAGGCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGAACATACATCA
CCACCTTCCTATGTCACATTGCACACAGCAGATTCCAGCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACACATA
CACCAATTGTCCTGTTCTGTGAAGAACTCTGACAAAATACAGATTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAATTGGTTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTATTACAATAATAAGATAGCAC
TATGTGTTAAA

FIGURE 54

MALLFSLILAICTRPGLASPSGVRLVGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVL
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGRHCKGRVEVKHQNWYTVCQTGWSLRAAKVVCRQLGGRAVL
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWCEDPFDLRLVG
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

T098E200-00600000

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACCGTCCGGACCGTGGCGGACCGTGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCCTGGG
CGTCTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGGGAAAGGCCAACCTGCCGAATGCTG
TGGTGGTGATCACAGGCCACCTCAGGGCTGGGAAAGAATGTGAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGAATGGTGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTGACCTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC
GACATACTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCAAGTGG
TGTGGACAAGAGGGTCAAGAGACAAACTACTTGGCCAGTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCCTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTG
CTGTCTCGTGGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCGGGATGGATCTAGGTATGGAGTTATGGAC
ACCACACAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTGGCTGTTATCTCGAA
CTCTGGCTCCTGGCTCTTCTGCAGCCTCATGGCCCTCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTGTTGAGACTTTAATGGAGATTGCTCTACAAGTGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAACGACAACA
AGCTTCTCCCAGGGTGAGGGAAACACTTAAGGAATAAATATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAGGGCGGCCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCATGGCCAACTTGGTTATTGCAAGCTTATAATGGTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVIITGATSGLGKECAKVFYAAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI
VAAAEEILQCFGYVDIL
VNNAGISYRGTIMDTTDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKS KNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGG**ATGAA**ATTCTTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTATTCTAA
GAGGAGAAAATCAGTCACCGGGAAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
GAUTGACTGCCTATGAATTGCTAAACTAAAGCAAGCTGGTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAATGCAAGGGACTGGGTGCCAAGGTTCATACCTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGACACATTCTGGACTACAAA
GGCATTCTTCTGCAATGACGAAGAATAACCATTGCCATATTGTCACTGTGGCTCGGCAG
CTGGACATGTCTCGGTCCCCTTACTGGCTACTGTTCAAGCAAGTTGCTGTTGGA
TTTCATAAAACTTGACAGATGAACGGCTGCCTACAAATACTGGAGTCAAAACAAACATG
TCTGTGTCCTAATTGTAACACTGGCTTCATCAAAATCCAAGTACAAGTTGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG
ATTTTATTCCATCTCTATAGCTTTAACACATTGAAAGGATCCTCCTGAGCGTT
CCTGGCAGTTTAAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA
AAGCGCA**ATAG**CACCTAGTTCTGAAAATGATTACCAAGGTTAGGTTGATGTCATCTA
ATAGTGCAGAATTAAATGTTGAACCTCTGTTCTAATTATCCCCATTCTCAATA
TCATTTTGAGGCTTGGCAGTCTCATTACTACCACTGTTCTTAGCCAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTAGAGGTGACTTAAGGAAAATGAAGAAAAAGAA
CCAAAATGACTTATTAAAATAATTCCAAGATTATTGTGGCTCACCTGAAGGCTTGCAA
AATTGTACCATAACCGTTATTAAACATATAATTATTATTGATTGCACTTAAATTGTT
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGGGTATTCAACATGAATATCATGAACCTCTCAATGGTAGGTT
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACCTCACATTCAATGCCAAACATTCT
GCACAGGGAAAGCTAGAGGTGGATACACGTGTGCAAGTATAAAAGCATCACTGGGATTAAAG
GAGAATTGAGAGAAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA
AA

FIGURE 58

MKFLLDILLPLLIVCSLESFVKLFI PKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETA AKCKGLGAKVHTFVVDCSNREDIYSSAKKVKA EIGDVSI LVNNAGVV
YTSDLFATQDPQIEKT FEVNVL AHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTS LGPTLEPEEVVNRLMH
GILTEQKMI FIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

TOP SECRET//COMINT//REF ID: A6260660

FIGURE 59

CCACCGCGTCCGGACCGTGGGCGACTAGTTAGATCGCGAGCGGCCGCCGCGCTC
AGGGAGGAGCACCGACTCGCCGCACCCCTGAGAGATGGTGGTGCCTATGGAAGGTGATTG
TTTCGCTGGTCTGTTGATGCCCTGGCCCTGTGATGGGCTGTTGCTCCCTATACAGAAGT
GTTCCATGCCACCTAACGGAGACTCAGGACAGCATTATTCCTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAAGGAAGAGAATTGAGTTGGTGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTGGTTC
TTCCCAGCTCAGATACAGCCAGAACGATGCCAGTAGTTCTGGCTACAGGGTGGGCCGG
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGCCCTATGTTGTCACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTACTGATGATAACCCACGGATATGCAGTCATGAGGACGATGT
AGCACGGGATTATACAGTGCACTAATTCAAGTTTCCAGATATTCCTGAATATAAAAATA
ATGACTTTATGTCACTGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGCAGAAATTCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAACAGCAGTGCCTGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCACTTAAC
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCGGT
GCACGGAACCTGAGGATCAGCTTACTATGAAATTGTCACTCCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGGAACTATAGTGAAGTACTTGCAGAGA
AGATACAGTACAGTCAGTTAAGCCATGGTTAATGAAATCATGAATAATTAAAGGTTCTGA
TCTACAATGCCAATGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCTGATGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGAATTCCATCAGGTAATTATTC
GAGGTGGAGGACATATTTACCCATGACCAGCCTCTGAGAGCTTTGACATGATTAATCGA
TTCATTTATGGAAAAGGATGGATCCTTATGTTGATAAAACTACCTCCAAAAGAGAACAT
CAGAGGTTTCAATTGCTGAAAAGAAAATCGAAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTCATATCTGCAAGATTTCATCAATAAAAATTATCCTGAAACAAAGTGAGC
TTTGTGTTGGGGGAGATGTTACTACAAATTAAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAATGA
AATTAAAGGTCTGAAATAGGAAGTTTAATTCTCTAAGAGTAAGTGAAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT
GTTGGAAATATTATGGATAAGAATAGCTCAATTATCCAAAATAAATGGATGAAGCTATAA
TAGTTTGAGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAACATTCTTGAAATA
AAAATATTATATAAAAGTAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGCDGLFRSLYRSVSMPPKGDSGQPLFLTPYIEAGKIQKGREL
SLVGPFGLNMKSYAGFLTVDNKTYSNLSFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPyVVTNSMTLRDRDFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLSLNPVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEEAFEILDKLLDGDLTSDPSYFQNV
TCNSYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGQTFNDGTIVEKYLREDTVQSVKPWL
TEIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYKGKWDPPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTCGGCTCCGAATGGCACATGTGGGAATCCCAGTCTTGGCTACAACAT
TTTCCCTTCTAACAAAGTCTAACAGCTGTTCAACAGCTAGTGTACAGGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAAGCTCCTTG
CCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCTGCCTAACAAAGCTTCAAAAAACAGGAGCGACTTCACACTGGCTGGGAT
AAGACGTGCCGGTAGGATAGGAAAGACTGGTTAGTCTTAATATCAAATTGACTGGCTGGG
TGAACCTAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTGTAAAATAAATTTAAAAAAGCAAGTATTGTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGGGAGAAAGTATGTTAAAATA
GAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAACCAAGGATGGGACCTGGTC
AGGCCAGCCTTTGCTCCTCCGGAAATTATTTGGTCTGACCACTCTGCCTGTGTTT
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
ACAGCCGCTCTGGTCTGCTCAGTGGCTGGGTGCTGCTGGCCCCCCCAGCAGCCGGC
ATGCCTCAGTCAGCACCTTCACTCTGAGAATCGTGAUTGGACCTCAACCACCTGACCGT
CCACCAAGGGACGGGGCGTCTATGGGGGCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCTCATCGTGCAGCCCTGAGCGAAGTGCTCACCCCTACCAACAATGTCAACAAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGAGCCTCTACCAGGGGTCTGCA
AGCTGCTGCCGCTGGATGACCTTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGACCATGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCTGTCCA
GCCGGAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCACTTGACAT
CTTCTACATCTACGGCTTGTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCCGAGA
CCCTGAGGGTGTGGCATCAACTCCGCTGGAGACCTCTCACACCTCACGCTCGTGG
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGTCCCTGCCCTCGGCTGCAACCGGGC
CGGGTGGAAATACCGCCCTCTGCAGGTGCTTACCTGCCAACGCTGGGACTCACTGGGCC
AGGCCTTCAATATCACCAGCCAGGAGGATGTACTCTTGCCATCTTCTCAAAGGGCAGAAG
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGTGCCCTCCATCCGGCATCAACTT
GCAGATCAAGGAGCGCCTGCAGTCTGCTACCAAGGGCAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGTCCAGTCACGAAGGCGCTGTCCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACCAGCCCTGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTG
TGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTAGCTAGATGCTCAATGCC
ATTCACCTCCTCAGCAAAGAGTCCCTTGGAAAGGTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTATTTCTGGGAACAAAGGTGAAATGGGAGGTAAGAAGGGTTAATTTGTG
ACTTAGCTCTAGCTACTTCCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCCAAACTTAAGAAAAACTTAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLTAAPLSMEQRQPWP
RALEVDSRSVVLSSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLLACGSL
YQGVCKLLRLDDLFLILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSACAFPIRAINLQIKERLQSCYQGEGN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGC GGACTGGAGTGGAAACCGGGTCCCCCGCGCTTAGAGAACACCGCGATGACCA
CGTGGAGCCTCCGGCGAGGCCGGCCCGCACCGCTGGACTCCTGCTGCTGGTCTTGGGCTTCTGGTGCCTCC
GCAGGCTGGACTGGAGCACCCCTGGTCCCTGCGGCTCCGCATCGACAGCTGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCACCTCTGGATCTCGGGGCTCCATCCACTATTCCTGCTGCCCCAGGGAGTACT
GGAGGGACCGCTGCTGAAGATGAAGGCCTGTTGAAACACCCCTCACCACTATGTTCCGTGGAACCTGCATG
AGCCAGAAAGAGGCAAATTGACTTCTCTGGGAACCTGGACCTGGAGGCCCTCGTCTGATGGCCGCAGAGATCG
GGCTGTGGTGAATTCTGCGTCCAGGCCCTACATCTGCAGTGAGATGGACCTGGGGCTTGCCAGCTGGCTAC
TCCAAGACCTGGCATGAGGCTGAGGACAACCTACAAGGGCTCACCGAAGCAGTGGACCTTATTGACCAC
TGATGTCAGGGTGGTGCACCTCCAGTACAAGCGTGGGGACCTATCATTGCGTGCAAGTGGAGAATGAATATG
GTTCTATAATAAAAGACCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGAACTGC
TCCTGACTTCAGACAACAAAGGATGGGCTGAGCAAGGGGATTGTCCAGGGACTTGGCCACCATCAACTTGCAGT
CAACACAGCAGCTGCAGCTACTGACCACCTTCTTCACACGTCCAGGGACTCAGCCCAGATGGTATGGAGT
ACTGGACGGGGTGGTTGACTCGTGGGAGGCCCTCACAAATATCTGGATTCTCTGAGGTTTGAAAACCGTGT
CTGCCATTGTGGACGCCGCTCTCCATCAACCTCTACATGTTCCACGGAGGCCAAACTTGGCTTCATGAATG
GAGCCATGCACCTCCATGACTACAAGTCAGATGTCAACAGCTATGACTATGATGCTGTGACAGAACCGGGCG
ATTACACGGCCAAGTACATGAAGACTCGAGACTTCTGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG
ACCTTCTCCCAAGATGCCGTATGAGCCCTAACGCCAGCTTGTACCTGCTCTGTGGACGCCCTCAAGTACC
TGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCT
TCGGGTACATTCTTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGATGTCAGTGGGGCAGG
TGTTGTGAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATGCTGTCCCCCTGATCCAGGGTT
ACACCGTGTGAGGATCTGGTGGAGAATCGTGGCGAGTCACATGGGAGAATATTGATGACCAAGCGCAAAG
GCTTAATTGAAATCTCATCTGAATGATTCAACCCCTGAAAAACTTCAGAACATCTATAGCCTGGATATGAAGAAGA
GCTTCTTCAGAGGTTGCCCTGGACAAATGGNTTCCCTCCAGAAACACCCACATTACCTGCTTCTTCTGG
GTAGCTTGTCCATCAGCTCCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGAGAAGGGGGTTGTATTCA
TCAATGGCCAGAACCTTGACGTTACTGGAACATTGGACCCAGAACAGCCTTACCTCCAGGTCCCTGGTGA
GCAGCGGAATCAACCAGGTACATGTTTGAGGAGACGATGGGGCCCTGCATTACAGTCAGGAAACCCCCC
ACCTGGGCAGGAACCAGTACATTAAGTGAGCGGTGGCACCCCTCTGCTGGTGCAGTGGAGACTGCCGCTC
CTCTTGACCTGAAGCCTGGTGGCTGCTGCCACCCCTCACTGCAAAGCCTCTGCAAGGAAAGGTGGATGGCTCTGGGCC
ACTGGGGGCTACAGTCTGCCCTGTCTCAGCTCAAACCTTAAGCCTGCAAGGAAAGGTGGATGGCTCTGGGCC
TGGCTTGTGATGATGGCTTCTACAGCCCTGCTTGTGGAGGAGGCTGTCGGGCTGTCTAGGGTGGAGC
AGCTAATCAGATGCCACGCCCTTGCCCTCAGAAAAAGTGTGAAACAGTGCCTTGTGGAGGCTTGCACAGCCC
TGCAGCATCTGCTGGACTCAGCGTGCTTTGCTGGTCTCTGGGAGGCTTGGCCACATCCCTCATGGCCCCAT
TTTATCCCCGAAATCCTGGGTGTGTCACCAGTGAGGGGTGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT
CTTCCCTCACACCTCTGAGCCTTCTGGATTCTGGAGGAACCTGGCGTGAGAACATGTGACTTCCCCCT
TCCCTCCCACTCGCTGCTCCCACAGGTGACAGGCTGGCTGGAGAACAGAACATCTCACCCTGCGTCTTCC
CAAGTTAGCAGGTGCTCTGGTCTGGTCACTGAGGAGGACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGCA
CATCCAGGGAGGAGGACAGAACGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGCAACATCC
AGGGAGGAGGACAGAACGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGCAACATCCAGGG
GGAGGACAGAACGCCAGCTCACATGTGAGTCCTGGCAGAACGCCATGGCCATGTCTGCAACATCCAGGGAGGAGG
ACAGAACGCCAGCTCAGTGGCCCCGCTCCCCACCCCCCAGGCCAACAGCAGGGGAGGAGCAGGCCACTGGCTTGGGCTACTGCTGA
GAAGTGTGTCCAAGTCCGATTGAGCCTGTTCTGGGGCCAGCCAAACACCTGGCTTGGGCTACTGCTGA
GTTGCAGTAAAGCTATAACCTGAATCACAA

FIGURE 64

MTTWSLRRR PARTL GLLL VVLGFLV LRR LDWSTL VPL RL R H R Q L G L Q A K G W N F M L E D S T F W
I F G G S I H Y F R V P R E Y W R D R L L K M K A C G L N T L T T Y V P W N L H E P E R G K F D F S G N L D L E A F V L M A
A E I G L W V I L R P G P Y I C S E M D L G G L P S W L L Q D P G M R L R T T Y K G F T E A V D L Y F D H L M S R V V P L Q
Y K R G G P I I A V Q V E N E Y G S Y N K D P A Y M P Y V K K A L E D R G I V E L L L T S D N K D G L S K G I V Q G V L A T
I N L Q S T H E L Q L L T T F L F N V Q G T Q P K M V M E Y W T G W F D S W G G P H N I L D S S E V L K T V S A I V D A G S
S I N L Y M F H G G T N F G F M N G A M H F H D Y K S D V T S Y D Y D A V L T E A G D Y T A K Y M K L R D F F G S I S G I P
L P P P P D L L P K M P Y E P L T P V L Y L S L W D A L K Y L G E P I K S E K P I N M E N L P V N G G N G Q S F G Y I L Y E
T S I T S S G I L S G H V H D R G Q V F V N T V S I G F L D Y K T T K I A V P L I Q G Y T V L R I L V E N R G R V N Y G E N
I D D Q R K G L I G N L Y L N D S P L K N F R I Y S L D M K K S F F Q R F G L D K W X S L P E T P T L P A F F L G S L S I S
S T P C D T F L K L E G W E K G V V F I N G Q N L G R Y W N I G P Q K T L Y L P G P W L S S G I N Q V I V F E E T M A G P A
L Q F T E T P H L G R N Q Y I K

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCAGGACC
CTGGTGAGGGTTCTACTTGGCCTTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGCTCGGCCGAGGCCCCCAGGACCTCCATCTCCAAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGGAGCGCTGTAAACGCCATGGCTCCC
AAGAAGCTGTCCTGCCTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTGTTCGTAGTGGATAGGGTCATGACCGGTTCTCCTAGACGGGGCCC
CGTCCGCTATGTCTGGCAGCCTGCACTACTTCGGGTACCGCGGGTCTTGGGCCGAC
CGGCTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGTCTATAACTTAATGGCAGGCCGACCTCATTGCCCTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCCATCCTGGTTGCTCGAAAACCTGAAATTCATCTAAGAACCTC
AGATCCAGACTTCCTGCCGAGTGGACTCCTGGTTCAAGGTCTGCTGCCCAAGATATATC
CATGGCTTATCACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGCTCTCCGTGACTGCTAGG
AGAAAAGATCTGCTCTCACACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GAECTATACCACTGTAGATTGGCCCAGCTGACAACATGACCAAAATCTTACCCCTGCTT
CGGAAGTATGAACCCCATGGGCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA
CTGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGAATTGG
AATGGTGCCGATAAGAAGGGACGCTCCTCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCACACCTAACGCTTTTGCTCTCGAGATGTCATCAGCAAGT
TCCAGGAAGTTCCCTGGGACCTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG
ACTCTGCACCTGGTTGGCATTACTGGCTTCTAGACTTGCTTGGCCCGTGGGCCAT
TCATTCAATCTGCCAATGACCTTGGCTGTCAAGCAGGACCATGGCTCATGTTGTACC
GAACCTATATGACCCATACCAATTGGAGCCAACACCAATTCTGGTGCCAAATAATGGAGTC
CATGACCGTGCCTATGTGATGGATGGATGGGTGTTCCAGGGTGTGGAGCGAAATATGAG
AGACAAACTATTTGACGGGAAACTGGGTCCAAACTGGATATCTGGTGAGAACATGG
GGAGGCTCAGCTTGGGCTAACAGCAGTGAACCTAACGGGCTGTTGAAGCCACCAATTCTG
GGGCAAACAATCCTACCCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTGTGAAGTG
GTGGTTCCCTCCAGTTGCCAAATGCCATATCCTCAAGCTCTTCTGGCCCCACATTCT
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGTTAACCTGGCCGGTACTGGACAAAGCAGGGCC
ACAACAGACCCCTACGTGCCAAGATTCTGCTGTTCTAGGGAGCCCTCAACAAAATTA
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGCACTGAAAGGTAGGCCGGCATGGTGCTCATGC
CTGTAATCCCAGCAGTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA
CCAGCCTGGCAACATGGTAAACCCGTCTCACTAAAAATACAAAAATTAGCCGGCGTG
ATGGTGGGACCTCTAATCCCAGCTACTGGGAGGCTGAGGGCAGGAGAATTGCTGAATCC
AGGAGGCAGAGGTTGCAAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTG
GACACTCCATCTCAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWQNHSTRSVAVTKGLENMLKLGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPGLPPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMHTTIFEPTFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRSLFGNSSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKKWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADETLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTGAAACACGTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACCTTGAAGGAATATT
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAACGATT
GCGTTCCCTTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGAGTTAGTGAAAATAACTTAGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGGTGCCGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCATTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCCTGCCTGGGTGTATTGCTCAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACATTACAGGAACGGAT
TTAAAGTCCAATAACATTGCACAATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT
GACTGTGTTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTTATTACCCATGTCA
AAAACTTGGAGTCACTTATTCTCTAACACAAGCTCGAACCTTACCAAGTGGCAGTATT
AGTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAAACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTAAATGCATAAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC
TCACCTCCAGAGAAAGTTGGTCAGCTCTCCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGTG
TGGAAGATCACCTTTGATAACCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAAATGGATTTAAACTAAGATAATATATGACAGTGTGAGTGCAGGAAC
AACTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATCTTTAAAATAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGAGGTTAAAGTCATTCAACATTGCTGATAGAAGGCTGATAGAAGACATAACTGAAT
AAAGGGAAGGAAAATTATAATCACTAATCTGGTTCTTTAAATTGTTGTAACCTGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLQRQHISRNAQDKQELHLFMLSG
VPDAVFDLTDLDVLKLELIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLESLRELRLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCELERIPHAIIFSLSNLQELDLKS
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTISSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCNDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACCGCGTCCGGCCTCTCTGGACTTGCATTCCATTCTTTGACAAACTGACTTTTTATTCT
TTTTTCCATCTCTGGGCAGCTGGGATCCTAGGCCGCCCTGGGAAGACATTGTGTTTACACACATAAGGAT
CTGTGTTGGGTTCTTCTTCCCTCCCTGACATTGGCATTGCTTAGTGGTTGTGTTGGGAGGGAGCCACGTGG
GCTCAGTGCTGCTGCACCTATCTGCCTAGGTACATCGAAGTCTTGACCTCCATACAGTGATTATGCCTGTC
ATCGCTGGTGTATCCTGGCCCTGCTCTGCTGATAGTGTGCTGCTGTCTTACTTCAAAATACACAAAC
GCGCTAAAAGCTGCAAAGAACCTGAAGCTGCTGCTGAAAAAAATCACAACCCAGACAAGGTGTGGTGGGCAAG
AACAGCCAGGCCAAAACCATTGCCACGGAGTCTGTGCTGCCCTGCTGAGGTGAGGATATAGAATGTGTGCC
AGTTTGATTCCCTGCCACCTTGCTGCGACATAAATGAGGCCCTTGAGTTAGGAAAGGCTCCCTCTCAAA
GCAGAGCCCTGAAGACTCAATGATGTCAATGAGGCCACCTGTTGTGATGTGCAAGGCCAGAAGAAAGGCCAG
CTCCCCATCAGTTCATGAAAATAACTCAGTGCTGGAACCCAGCTGCTGGAGATCCCTACAGAGAGCTC
CACTGGGGCAACCCCTCAGGAAGGAGTTGGGAGAGAGAACCCCTCACTGTGGGAATGCTGATAAAACCAGTCA
CACAGCTGCTCTATTCTCACACAAATCTACCCCTGCGTGGACTGACGTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCCTATAAAAGCTGTCGGTCTTAAGGCTGCCAGGCCCTGCAAAATGGAGCTGTA
AGAAGGCTCATGCCATTGACCCCTTAATTCTCTCTGTTGGCGAGCTGACAATGGGGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTGCCTAATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAGACCAAAACAAAGCATCAGAATTATCTTCTATGTCCAGCTT
GATCCAGATGGAAGCTGTAAGGATGAAAACATTAAAGTCTTGACGGAACCTCCAGCAATGGGCTCTGCTAGGG
CAAGTCTGCAGTAAAAGACTATGTCCTGTATTGAATCATCATCCAGTACATTGACGTTCAAATAGTTACT
GACTCAGCAAGAATTCAAAGAACTGCTTTGTTCTACTACTTCTCTCTAAACATCTTCTATTCCAAACTGT
GGCGGTTACCTGGATACCTTGGAGGATCCTTACCCAGCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT
TGTGTTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTCAAAGAGATTTCCTAGAAATAGAC
AAACAGTGCCTTCTGCACTATGATGGCCCTCCACCAACTCTGGCTGATTGGACAAGTCTGT
GGCGTGTGACTCCACCTCGAACATCGTCATCAAACCTCTGACTGTCGTGTTCTACAGATTATGCCATTCT
TACCGGGATTCTGCTCTACACCTCAATTATGAGAAAACATCAACACTACATCTTAACTTGCTCTTCT
GACAGGATGAGGTTATTATAAGCAATCTACCTAGAGGTTAACTCTAAATGGGAATAACTTGCCTAACTAAA
GACCCAACTTGCAGACCAAAATTATCAAATGTTGGAATTCTGCTCCCTCTTAAATGGATGTTGACAATCAGA
AAGGTAGAAGATCAGTCATTACTACACCAATAATCACCTTCTGCACTCTCAACTTCTGAAGTGATGAC
CGTCAGAAACAACCTCCAGATTATTGTAAGTGTGAAATGGACATAATTCTACAGTGGAGATAATACATAACA
GAAGATGATGTAATACAAAGTCAAATGCACTGGCAAAATAACACCAAGCATGGCTTTTGAATCCAATTCA
TTTGGAAAAGACTATACTGAAATCACCATTATGTTGAACTTTGTTGTCAGTTAGTCTGCAC
ACCTCAGATCCAAATTGTTGTTCTGATACCTGTAGGCCCTCCACCTCTGACTTTGCACTCTCAACC
TACGACCTAATCAAGAGTGGATGTAAGTGTGAGATGAAACTGTAAAGGTGTATCCCTTATTGGACACTATGGGAGA
TTCCAGTTAATGCCCTTAATTCTGAGAAGTATGAGCTGTGTATCTGCACTGTAAAGTTGATATGTGAT
AGCAGTGACCACCAAGTCTCGCTGCAATCAAGGTTGTGTCCTCAGAAGCAAACAGAGACATTCTCATATAATGG
AAAACAGATTCCATCATAGGACCCATTGTCGAAAAGGGATGCAAGTGCAGTGGCAATTCAAGGATTCAGCAT
GAAACACATGCCAGAAACTCCAAACCAAGCCTTCAACAGTGTGCACTGTTTCTCATGGTTCTAGCTCTG
AATGTGGTACTGTAGCGACAATCACAGTGAGGCATTGTAATCAACGGGAGACTACAAATACCAGAAGCTG
CAGAACTATTAACTAACAGGTCCAACCTAAGTGAGACATGTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATTATGAATAATGAGGAAGGGCTGAAAGTGACACACAGGCCCTGCATGTA

FIGURE 70

MELVRRLLMPLTLLLILSCLAEITMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIFSYVQLDPDGSCESENIKVFDGTSSNGPPLLQVC SKNDYVPVFESSSSTLT
FQIVTDSARIQRTVFVFFYFFSPNISIPNCGGYLDTLEGSFTSPNPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDQCKFDLAIYDGPSTNSGLIGQVCGRVTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTIILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL
QCKVLI CDSSDHQSRCNQGCVRSRSKRD ISSYKWKTD SII GPIRLKRD RSASGN SGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383, 408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-233

Prokaryotic membrane lipoprotein lipid attachment site

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCCCAGGAGCTCCCAGGCTCGCGTTCCCGTGTGCTGTTGCTGCTGC
TGCTGCCGCCGCGCCGTGCCCTGCCACAGCGCCACCGCGCTCGACCCCACCTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGCGTGGTTGACCAGGCCAAGTCGGCATCTTCATCCACTG
GGGAGTGTTCGCCCAGCTCGGTAGCGAGTGGTCTGGTGGTATTGGCAAAAGGAAA
AGATACCGAAGTATGTGAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT
TTTGGACCACTATTACAGCAAAATTTTAATGCCAACAGTGGGCAGATATTTCAGGC
CTCTGGTGCAAATACATTGCTTAACCTCCAAACATCATGAAGGCTTACCTTGTGGGGT
CAGAATATTGTGGAACCTGGAATGCCATAGATGAGGGCCAAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTGGACTGTACTATTCCCTTTGA
ATGGTTTCACTCGCTTCTGAGGATGAATCCAGTCATTCCATAAGCGGCAATTTCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATCAGCCTGAGGTTCTGTGG
TCGGATGGTACGGAGGAGCACCGGATCAAACTGGAACAGCACAGGCTCTGGCCTGGTT
ATATAATGAAAGCCAGTTGGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTACCTGCAGTGATCGTTATAACCCAGGACATTTGCCA
CATAAATGGGAAACTGCATGACAATAGACAAACTGTCCTGGGCTATAGGAGGAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTCATGTG
GAGGAAATCTTGATGAATATTGGCCCACACTAGATGGCACCATTCGTAGTTTGAG
GAGCGACTGAGGCAAGTGGGCTCTGGCTAAAAGTCATGGAGAAGCTATTGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTCTAAATGGCCCACATCAGGACAGCTGTTCTGGCCAT
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAAC
GATTCTTGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCAGATGC
CGTGTAAATGGGCTGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGAAACTGGATAAGAAAATTATGGCAGTTCAAGCCCTTCCCTTTCCACTA
AATTCTTCTAAATTACCCATGTAACCATTAACTCTCCAGTGCACTTGCCATTAAAGTC
TCTTCACATTGATTGTTCCATGTGACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTATGTTGAAGCCATATCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAT
TTTTTTGTGCCAACATCATAGAGTGTATTACAAAATCTAGATGGCATGCCACTACA
CACCTAATGTGTATGGTATAGACTGTCCTAGGCTACAGACATATAAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAAACTGTAAAATAATGGTGACCTGTATAGGGCACTTACCAAGGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAAACTGTATGCTTAGGCTACACTACATTATAAAAAAAA
GTTTTCTTCTTCAATTATAAATTAAACATAAGTGTACTGTAACCTTACAAACGTTTAATT
TTTAAAACCTTTGGCTTTGTAATAACACTAGCTTAAACATAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPPCAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWCNCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKEKLVYAIIFLKWPMSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTTCCATCTGGACCAAGGCTCTGGTCAAGGCTTTGCGTGAGAAGAGCT
TTCCATCCAGGTGTCATGCAGAATTATGGGATCACCCCTGTGAGCAAAAGGCGAACAGC
AGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAACACTGCAGCTATGGCTGGGTTGGAGA
TGGATTCGTGGTCATCTCTAGGATTAGCCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTG
TCCTGATTGGAAAGGTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACACTCATCTGAT
ACTTGGACTAACTCGTGCAATTCCAGAAATTATCACCAACAAAGATCCCATTCAACACTCA
AACTGCAACACAAACAGAATTATTGTCAAGTACAGTACCTACTCGTGGCATCCCCCTT
ACTCTACAATACCTGCCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTCACAGAAGTTTATGAAACTAGCACCATGTCTACAGAAAC
TGAACCATTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTC
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGAGCTGGCTTGAGATTTC
TATGTCAAAAGGTATGTGAAGGCCTCCCTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTAATGAGGAATCAAAGA
AAACTGATAAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACCTACCGTGCATGCCTGGAA
GCTGAAGTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC
TTACCTGCCAGCTGGGAAATCAAAGGCCAAGAACCAAAGAAGAAAGTCCACCC
GGTTCCCTAATGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC
CCTTCTCCTATTGTAACCCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCACGGCC
TTCTAGCCTGGCTATGTCTTAATAATATCCACTGGGAGAAAGGAGTTTGCAAAGTGCAA
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGAC
CCTTCTCAGCTCTGAAAGAGAAACACGTATCCCACCTGACATGTCTCTGAGCCGGTA
AGAGCAAAGAATGGCAGAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAGCTAAAATAAAGAAATAGAACAAAGCTGAGGATAACGACAGTACACT
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTGAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTTCT
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAATTCTATTGAGACT
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGCAAGGTATTACACTCTGTAAT
TGAATTATTCTCAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTGTTCT
GTTTGATATTCTAGCTTACTCTTCCAAACTAATTGTTATTGCTGAGACTAATCTT
ATTCAATTCTCTAATATGGCAACCATTATAACCTTAATTATTAAACATACCTAACAG
TACATTGTTACCTCTATATACCAAAAGCACATTAAAAGTGCCATTAACAAATGTACT
GCCCTCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAATTAA
AGCATTAGAAAATT

FIGURE 74

MARCFSLVLLLTSIWTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNSPKCGKNGVGVLIWKVPVSRQF
AAWCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAASKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFTPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTATTGGTGCACGACTTACGATGG
CTCGCCAACCTTACTACCTCTGTCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA
ACTGCCGCCGCTCTGCCACGGCTGCCACCCAACGCGAAGACGGTAACCGTGTGACTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACATAGAACGGACAAGAGGGTCACGGATTGTGGAGTTCTTGCAA
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTTGGAAAGGTGGATGTTGGACGCTACTGATGTTAGTACGGTAC
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCCTGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTCG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACCACAGTGTCA
TGGGAAAACAAGAAGGATAAAAGATCCTACTTGGCAGTGCTCCTCTCGTCAATT
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTCCCTTGG
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTTAAAGAGGCATCTAGGGATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCCAAGTGGACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGGAAATGGTTCCCTCCAAGCTGGTCAGTGTGTTACTGCTTATC
AGCTATTAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCCCTTAG
TTGACCTGCACAGCTGGTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTTCACCCAGGACTCTGCTCCTTAAGCCCTCTGGCTCGTTATGGTC
TTCATTAAAAGTATAAGCCTAACCTTGTGCTAGTCCTAAGGAGAAACCTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCCCTATTGTGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGGTAGGACTTGGAGGAGAAATCCCTGGACTTCAC
TAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGCGCCCCGAGAGCTAGCCGTCGAGGAGCTGCCCTGGGACGTTGCCCTG
GGGCCCCAGCCTGGCCGGGTACCCCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCCA
TTGCTCCTGCTGCCCGGCTCCTACGGACTGCCCTCTACAACGGCTTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTACGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCCTGTTCACCTACCAAGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGGCGGTGCGTGTCAAATGGTGGAAAGCT
GTCGGAGAACGGGGCCCCAGAGAACGGACGTGCTGGTGGCCATCGGCTGAGGCACCGCTCCT
TTGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTCGGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTCAATTGACGGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGCTTTCTTACCAAGTCCCCCA
ACGGCGCTACCACTCAACCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCCGTG
GTGGCCTCCTTGAGCAGCTCTCCGGGCTGGAGGAGGGCCTGGACTGGTGCAACGCCGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCCGTGGC
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACCGCCGCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCCCTGAGAACG
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC
AGCTTTGCCGCCTGGAAAGTCCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCCTGTGGTCACCCGCATCCTAACTGTGGCCCCCAGAGCCTGGG
CCGAAGCTTGGCTCCCCGACCCGCAGAGCCCTGTACGGTGTACTGCTACCGCCAGC
ACTAGGACCTGGGCCCTCCCTGCCGCATTCCCTACTGGCTGTGTATTATTGAGTGGTT
CGTTTCCCTGTGGGTGGAGCCATTAACTGTTTATACTTCTCAATTAAATTCT
TTAACATTTTTACTATTTTGAAAGCAAACAGAACCCATGCCCTCCCTTGCTCCTG
GATGCCCACTCCAGGAATCATGCTTGCTCCCTGGGCCATTGCGGTTTGCGCTTCTG
GAGGGTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCCTGG
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGCATGGTGGCACAGTCTCCCTGCC
CAGCCTGGGGAAAGAACGGGCCTGGGGCCTCCGGAGCTGGCTTGGCCTCCTGCC
CACCTCTACTTCTGTGAAGCCGCTGACCCAGTCTGCCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGGCGAAATCTGAGGAAAGGAAGAACCTCCCTCCCCGTTCC
TCCCTCTCGTTCCAAAGAATCTGTTGTGTCATTGTTCTCCTGTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGCTATGACTGCCCTCCGCC
AA
AA

FIGURE 78

MGLLLLVPLLLPGSYGLPYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEELDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGP
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG**GATGAT**GTGGCGACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGGGGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGGAA
CTTCCAGTACGACCATGAGGCTTCCTGGGACGGGAAGTGGCAAGGAATTGACCAACTCA
CCCCAGAGGAAAGCCAGGCCGTCTGGGCGGATCGTGGACCGCATGGACCGCGCGGGGAC
GGCGACGGCTGGGTGTCGCTGGCCGAGCTCGCGCGTGGATCGCGCACACGCAGCAGCGCA
CATACGGGACTCGGTGAGCGCGGCCTGGACACGTACGACACGGACCGCGACGGCGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGCCACTACGCGCCCGTGAAGAATTGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTGGGACGAGCGGCGTTCCGGTGGC
CGACCAGGATGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTCCTGCACCCCGAGG
AGTCCCTCACATGCGGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTCCGGACTTCCGGATCTGAACAAGG
ATGGGCACCTGGATGGAGGTGAGGTGGCCACTGGGTGCTGCCCTGCCAGGACCAGCCC
CTGGTGGAAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAA
AGCGGAAATCCTGGTAATTGGAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACACGATGAGCTG**TGAG**CACCGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACCGGAGGAGGGGCCGCTGGTCTGGCCCTCCCTGTCCAGGGACCCCTGGGTGGCTTC
GCAGATGCAGTCCCAGGCATCCTCCTGCCCTGGCTCTCAGGGACCCCTGGGTGGCTTC
TGTCCCTGTCACACCCCCAACCCAGGGAGGGCTGTCATAGTCCCAGAGGATAAGCAATAC
CTATTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTGGCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCAAATCTGAGCCTCCACCATAGACTGAAACTCCCCT
GGCCCCAGCCCTCTCCTGCCTGGCCTGGACACCTCCTCTGCCAGGAGGAATAA
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSPDAGPHQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDGRVGWEELRNATYGHYAPGEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKGHDGSEVGHVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTGCCCTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCAGGGCGCGGGTGCAGGGGATCCCTGACGCCCTCTGTCCTGTTCTTGTGCGCTCCCAG
CCTGTCTGTCGCTGTTGGCGCCCCCGCCTCCCGCGGTGCGGGGTTGCACACCGATCCTG
GGCTTCGCTCGATTGCGCCGAGGGCGCTCCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG
CGGGTCGCTGTGTCCTCTCCTCTGCGCCGCCCGGGATCCGAAGGGTGCAGGGGCTCT
GAGGAGGTGACGCGCGGGCCTCCCACCCCTGGCCTGCCCCTGCATTCTCCCTCTCCCAG
GTGTGAGCAGCCTATCAGTCACCATGTCGCAAGCCTGGATCCCAGCTCGGCCTCGGTGTG
TGTCTGCTGCTGCCGGGCCGCGGGCAGCGAGGGAGGCCGCTCCCATTGCTATCACATG
TTTACACAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGCTGCC
CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTCTGTATCGAGCATATGTGG
GCTGCTGTCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC
TGGTCGAGAAAACATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT
GGTCTGCTCTTCACAGTAACAAAGCAGGAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAACAGACTAAAGAAAACACCCAGAGAAGAAAAC
CAATAAAGATTGTAAGCAGACATTGCATTCTGATTGATGGAAGCTTTAATATTGGCAGC
GCCGATTAAATTACAGAAGAATTGGCTCTAATGTTGGAAATTGGCTCTAATGTTGGAAATTGG
GAAGGACCACATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATTACTTGAA
AAACTTACATCAGCAAAGATGTTGTTGCCATAAGGAAGTAGGTTCAAGGGGTTA
ATTCCAATACAGGAAAGCCTTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTATTATTGATGGTGGCCTTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTCTTACACATGCCAACTGGTTGGCACCACAAAATACGTAAA
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAAGACCTGTTATAACT
CAGTGAACATTGCCCTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCC
ATGCTTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTGCAAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCACTGACTATAGCACCA
AAGAGAATGTCCTAGCTGTCACTAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGG
GATGCCATTCCCTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCCTAGTAATTGTCACAGATGGGAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG
CACATGATGCAGGAATCACTATCTCTGTGGTGTGGCTTGGCACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTCTTACAAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGTTAGAGATTCTTAGAAATCCCAGCAAT
AATGGTAACATTGACAAC**TGAAAGAAAAAGTACAAGGGGATCCAGTGTGTA****ATTGTATT**
CTCATAATACTGAAATGCTT**TAGCATACTAGAATCAGATA****ACAAAACATTAAAGTATGTCAAC**
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCTCTGGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAAACTCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAA
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLEFSVY
GNIVYASVSSICGAAVHRGVISSNGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCCKADIAFLIDGSFNIQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRMLFEVSNIAKTFEISDIGAKIAAVQFTYDQRTESFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCCGCGCTCCCGCACCCGCGGCCGCCACCGCGCCGCTCCGCATCTGCACCCGCAGCCC
GGCGGCCTCCGGCGGGAGCGAGCAGATCCAGTCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCG
GGCGGGCGGCTGCGGGCGCAGAGCGGAGAT**GCAGCGGCTTGGGCCACCCCTGCTGTGCCTGC**
TGCTGGCGGGCGGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTC
AAGCCCGGCCGGCTCTCAGCTACCCGAGGAGGAGGCCACCCCTCAATGAGATGTTCCGCGA
GGTTGAGGAAGTGTGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACATTACCTCCAGCTAT
CACAATGAGACCAACACAGACACGAAGGTTGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTAAGTGCAGTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTCTGGGTCACTGCACCAAAA
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG
TGCTGTGCCTCCAGAGAGGCCTGCTGTTCCGTGACACCCCTGCCGTGGAGGGCGA
GCTTGCCATGACCCGCCAGCCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG
GAGCCTGGGACCGATGCCCTTGTGCCAGTGGCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTTCGTGGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGGCAGCTTCACTGGAGGGAGGTGCCAGGAGCTGG
AGGACCTGGAGAGGAGGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGTGCCGCT
GCACTGCTGGAGGGAGAGATT**TAGAT**CTGGACCAAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTCCCCAGGTGTGCTTAGGCGTGGCTGACCAGGCTTCTTACA
TCTTCTTCCCAGTAAGTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTCATTGTTCA
TCCCCCAGGCTGTTCTCAGGCTCACAGTCTGGCTTGGGAGAGTCAGGCAGGGTTAAC
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCACAGTTGGCAG
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGGAAACAATGTGG
AGTCCTCTCTGATTGGTTGGGAAATGTGGAGAAGAGATGGCCCTGCTTGCAAAACATCAA
CCTGGCAAAATGCAACAAATGAATTTCACCGCAGTTCTTCCATGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGAGATGAAATGTTCTGTTCACCCGCATTACATGTGTTATTCATCC
AGCAGTGTGCTCAGCTTACCTCTGCCAGGGCAGCATTTCATATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGGGGAGGGGTATTGTTCTCCTCGTCCATAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTTGCCTAACAGTCAACAGCTAGTGAAGACAGAGCAGTT
CTGGTTGTGACTCTAACGCTCAGTGTCTCTCCACTACCCCCACACCAGCCTGGTGCCACCAA
AAGTGTCCCCAAAAGGAAGGAGAATGGGATTCTTGAGGCATGCACATCTGGAATTAAAG
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCCGTCTTCTAATGAAGACAAATGATATTGACACTGTCCCTCTTGGCAGT
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATACTGGTTAACCTGCAGAAC
GTACTTAGTAATTGTAGGGCGAGGATTATAAATGAAATTGCAAACACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACCTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTGACAGTTCTTAAAGTTAAAGTTGACATGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTTGCATTAGAAATCAAGC
ATAAAATCACTCAACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLNLPPSYHNETNTDTKGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPGASGLLQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVVRQELEDLERSLTEEMALGEPAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCTG
AAGATAACAATAATTTCAGCCCCATCCACTCTCCCTCCCAAACACACATGTGCATGTACACACACACATACA
CACACATACACCTCTCCTCCTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCAAGAAAAGGACAC
TAAAGCCTTAAGGACAGGGCTGGCATTACCTCTGCAGCTCTGGCTGTGAGTCAGAAAACATGGGAGGG
CCAGGCACGGTGAACACCTGTAATCCCAGCATTTGGGAGACCGAGGTGAGCAGATCACTTGAGGTCAAGGAG
TTCGAGACCAGCTGGCAGATGGAGAAACCCCCATCTACTAAGAAAATAGCCAGGAGTGGTGGC
AGGTGCCTGTAATCCCAGTCACTCAGGTGGCTGAGCAGGAGAATCGCTGAATCCAGGAGGGAGGATGCAGT
CAGCTGAGTGACCGCTGCACCTCCAGGCTGGGTGACAGAAATGAGACTCTGTCTCAAACAAACACGGGAGGA
GGGGTAGATACTGCTTCTGCAACCTCTTAACCTCTGCATCCTCTTCCAGGGCTGCCCTGATGGGGCTG
GCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGA
GTGTAGAAATGACTGCCCTGGGAGGGTGGTCCCTGGGCCCTGGCAGGGTTGCTGACCCATTACCTGCAAAACACA
AAGAGCAGGACTCCAGACTCTCTTGTGAATGGTCCCCTGCCCTGAGCTCCACCAATGAGGCTTCTCGTGGCCCC
ACTCTTGTAGCTGGGTTGGCTGGTGCCTGCCACTGCCACTGTGCCGTGGTACCCCTGGCATGTTCCCTGCC
GTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCGCTGTCCTACCGCGAGGCTACCACTGTGGACTGCAATGA
CCTATTCTGACGGCAGTCCCCCGGCACTCCCCGCAAGGCACACAGACCCCTGTCCTGAGAGCAACAGCATTGT
CCGTGTGGACCAGAGTGAGCTGGGCTACCTGGCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTGG
TGCCCGAGACTGTGATTTCATGCCCTGCCAGCTGCTGAGCCTGCACCTAGAGGAGAACAGCTGACCGGCT
GGAGGACCACAGCTTGCAAGGCTGCCAGCTACAGGAACCTATCTCAACCACAAACCAGCTTACCGCATTGC
CCCCAGGGCTTTCTGGCTCAGCAACTTGCTGCCGTGCACCTCAACTCCAACCTCTGAGGGCATTGACAG
CCGCTGGTTGAAATGCTGCCAACCTGGAGATACTCATGATTGGGGCAAAAGGTAGATGCCATCTGGACAT
GAACCTCCGGCCCTGGCAACCTGCGTAGCCTGGTCTAGCAGGCATGAACCTGCCGGAGATCTCGACTATGC
CCTGGAGGGCTGCAAAGGCTGGAGAGCCTCTCTTCTATGACAACCAAGCTGCCGGGTGCCAGGGCACT
GGAACAGGTGCCGGGCTCAAGTCTCTAGACCTCAACAAGAACCCGCTCCAGGGTAGGGCCGGGGACTTGC
CAACATGCTGCACTTAAGGAGCTGGGACTGAACAAACATGGAGGAGCTGGTCTCCATCGACAAGTTGCC
GAACCTCCGGAGCTGACCAAGGCTGGACATCCAATAACCCACGGCTGTCCTCATCCACCCCCGGCCTCCA
CCACCTGCCCTGAGATGGAGACCCCTCATGCTCAACAAACAGCTCTAGTGCCTGCCAGCAGACGGTGGAGTC
CCTGCCCAACCTGCAAGGAGGTAGGCTCTCACGGCAACCCCATCGCTGTGACTGTGTCATCCGCTGGCA
CACGGGCACCCGTGCGCTTCATCGAGGCCAATCCACCCCTGTGCGGCCACTCCAGCGCCTCCC
GGTCCTGAGGTGCCCTCCGGAGATGACGGACACTGTTGCCCTCATCTCCCAAGAACGCTTCCCCCAAG
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCATTGCCGGCACTGCCGAACCCGAACCCGAGATCTACTG
GGTCACTCCAGCTGGCTTCGACTGACACCTGCCATGCAGGCAGGGTAGGGGTACCCGTGACCCGAGGGAC
GGAGCTGCCAGGGTACAGCAGAAGAGGCAGGGCTATACACCTGTGTCGCCAGAACCTGGTGGGGCTGACAC
TAAGACGGTTAGTGTGGTGTGGCCGTGCTCTCCAGCCAGGCAAGGGAGGAAGGACAGGGGCTGGAGCTCG
GGTGCAGGAGACCCACCCCTATCACATCTGCTATCTGGTCAACCCACCCAAACAGTGTCCACCAACCTCAC
CTGGTCCAGTGCCCTCCCTCCGGGCCAGGGGCCACAGCTGGCCCGCTGCCCTGGGAACCCACAGCTA
CAACATTACCCGCTCTTCAGGCCACGGAGTACTGGCCTGCCATGCAAGTGGCCTTGTGATGCCACACCA
GTTGGCTTGTGATGGGCCAGGACAAAGAGGCCACTCTTGCACAGAGCCTAGGGGATGTCCTGGCTCAT
TGCCATCCTGGCTCTGCTCTGCCAGCTGGCTAGGCCACCTTGCAAGGCCAACCCAGGAA
GGGTGTGGTGGGAGGGCGCTCTCCAGGCTTCTGGGCTTCTGGGCTGGAGTGCCCTTCTGTCCGGTTGT
GTCTGCTCCCCCTGCTCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGACACTGTTGCC
ACCATTGTCTAAAATCTGAGCTCAGCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTACAAA
AGAGAAGCAGTCTGGCCAGATGCCCTGCCAGGAAGGGACATGGACCCACGTGCTGAGGCCAGCTGGC
CAAGACAGATGGGGCTTCTGGGCCCTGGGGCTGCTCTGAGCCTTGAAGAAAAGTGCCTTACCTCTAGGGTCA
CCTCTGCTGCCATTCTGAGGAACATCTCAAGGAACAGGGAGGACTTGGCTAGAGCCTCTGCCCTCCCATCTT
CTCTCTGCCAGGGCTCTGGGCCCTGGCTGTCCTGCTGCTCTGGCAAGGGCTGAAGGAGGCCACTCCATCTCAC
TCTTTCTGTACAGTCTCAGTTGCTTGTGCTCTGGCAAGGCTGACTTTCTATAGGCAATTGTACCTTGTGGAGAA
CTCGGGGGCTGCCCTCAATGTGGAGTGACCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAA
CGCCTCATCTCAGCAGCCTGGCTGGCATTCCGAAGGCTGACTTTCTATAGGCAATTGTACCTTGTGGAGAA
ATGTGTACCTCCCCAACCGATTCACTCTTCTCTGTAAAAAATAAAATAACAATAAAA
AAAA

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLQLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMNFRPLANLRSILLAGMNLREISDYALEGLQSLSESLSFYDNQ
LARVPRRALEQVPGLKFLDLNKNPLQRVPGDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNPRLSFIHPRAFHHLQPQMETLMLNNNALSALHQQTVESLPNLQEVLHGPNIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLERRVTAEEAGLYT
CVAQNLVGDATKTVSVVGRALLQPGDRDGQGLELRVQETHPYHILLSWTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLAAHLGTGQPRKGVGGRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPSSGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GAAGGCCAAGGCCTGTTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGGGGACATTGTGACCGCCT
CTACATGGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGACCAA
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCACCC
CCTGGCCACACTCTTCAAGATCCTGGCTCCTTACATCAGCCTAGTCATCTTCTACGGCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCCTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCTTACGCTGCACCTCATTGACCAATACGACCCGCTACTCCAA
GCGCTTCGCCGTCTTCTGCGAGGTGAGTGAGAACAGCTGCCAGCTGAACCTCAACAACGAGTGGACGCT
GGACAAGCTCCGGCAGGGCTACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTTATGCTCAGTGGCAT
CCCTGACACTGTGTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCC
CAGCATTGCCAGCTCACGGCCTCAAGGAGCTGTGGCTTACACACAGCGGCAAGATTGAAGCGCTGCGCT
GGCCTTCTGCGGAGAACCTGGGGCGCTGCACATCAAGTCACCGACATCAAGGAGATCCCGCTGTGGATCTA
TAGCCTGAAAGACACTGGAGGAGCTGCACCTGACGGCAACCTGAGCGGGAGAACAAACGCTACATCGTCA
CGGGCTGGGGAGCTCAAACGCTCAAGGTGCTGGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGTGGTCA
AGATGTGGGCGTGCACCTGCAAGAGCTGTCATCAACAATGAGGGCACCAAGCTCATGTTCTCAACAGCCTCAA
GAAGATGGCAACCTGACTGAGCTGGAGCTGATCCGCTGCCACCTGGAGCGCATCCCCACTCCATCTTCAGCCT
CCACAACCTGCGAGGAGATTGACCTCAAGGACAACACCTCAAGGACCATCGAGGAGATCATCAGCTTCAGCACCT
GCACCCGCTCACCTGCTTAAGCTGTGTTACACACATGCCATCCCCATCCAGATCGGCAACCTCACCAA
CCTGGAGCGCTCTACCTGAACCGCAACAGATCGAGAAGATCCCCACCCAGCTTCTACTGCCGCAAGCTGCG
CTACCTGGACCTCGCCACACAAACCTGACCTTCTCCCTGCCGACATGCCCTCTGAGAACCTCCAGAACCT
AGCCATCAGGCCAACCGGATCGAGACGCTCCCTGGAGCTCTCCAGTGGGGAGCTGCGGGCCCTGCACCT
GGGCAACAAACGTGCTGCAGTCACTGCCCTCCAGGGTGGCGAGCTGACCAACCTGACGAGATCGAGCTGGGGGG
CAACCGCTGGAGTGCCTGCTGTGGAGCTGGCGAGTGCCACTGCTCAAGGCCAGGGCTTGGTGGAGGAGA
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCTGAGCAG
GCCGGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCGGAGGGCAGGCTAGCTTCTCCAG
AACTCCGGACAGCCAGGACAGCCTCCGGCTGGCAGGGAGCTGGGGCTTGTGAGTCAGGCCAGAGCAGA
GGACAGTATCTGTGGGCTGGCCCTTCTCCCTCTGAGACTCACGTCACCCCCAGGGCAAGTGTGTTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGTCTCTCCCTGGAGGCCAGCTGCCCCAGGGCTGAG
CTGCCACCAGAGGTCTGGGACCTCACTTTAGTTCTGGTATTATTCTCCATCTCCACCTCCTCATCC
AGATAACTTACATCCAAAGAAAGTTCAGCCAGATGGAAGGTGTTAGGGAAAGGTGGCTGCCCTTCCCC
TTGTCTTATTAGCGATGCCCGGGCATTAAACACCCACCTGGACTTCAGCAGAGTGGCCGGGGCAACAG
CCATGGGACGGTCACCCAGCAGTGCCTGGCTCTGCGGTGCGGTCCACGGGAGAGCAGGCCCTCAGCTGGA
AAGGCCAGGCCCTGGAGCTGCCCTTCAGTTTGTGGCAGTTAGTTTTGTGTTTTTTTTTAATCAA
AAACAATTTTTAAAAAAAGCTTGAAATGGATGGTTGGTATTAAAAAGAAAAAAACTAAAAAA
AAAAGACACTAACGCCAGTGAAGTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTTGAGCAAAGCAGGCCAGACGT
TGAAGTGTGTTCTTCCCTGGCGCAGGGTGCAGGGTGTCTTCCGGATCTGGTGTGACCTGGTCCAGGAGTT
CTATTGTTCTGGGAGGGAGGTTTTTTGTGTTTTGGGTTTTGGTGTCTTGTGTTCTTCTCCTCC
ATGTGTCTGGCAGGCACTCATTCTGTGGCTGCCAGGGAAAGTGTCTGGAGCTGCCAAGGGAGGAG
ACTCGGGTCTGGCTAATCCCCGGATGAAAGGTGCTCAGGCCACCTCCCTCTGGCTGCCCTGCCCTC
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTTCGCCAGACTTGTCTTCCCTCTGGCAGGGCATGGTGTG
CCAGTGCCACCGCTGGCCTCCGCTGCTTCCATCAGCCCTGCGCACCTGGTCTTCAAGGAGCAGACACTTA
GAGGCTGGTGGGAATGGGGAGGTGCCCTGGAGGGCAGGGCAGGGCTGGTCTTCAAGGCCGTTCCCGTCTGGCG
CTGGAGTGCACACAGCCAGTGGCACCTGGTGGCTGGAAAGCCAACCTGCTTGTAGATCAGTGGTCTCC
AGAAGGGTCCCCGCCCTAGATCAATCAGTGGACACTAAGGCACGTTTAGAGTCTCTGTTAATGATTATGT
CCATCCGTCTGCGTCCATTGTGTTCTGCGTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGAAAAATCCGTTACATGTGGGCTGAACTGTAGACTCGGTACAGTATCAAATAA
ATCTATAACAGAAAAAA

FIGURE 88

MRQTIIKVIKFILIIICYTVYYVHNIKFVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNLNEWTLDKLRQRLTKNAQDKLELHLFMLSGIPDTVFVFLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFDTIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHGNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCATACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACCTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTTGGAAACTTGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT
GTGGATAATCCC GTGGGCACTGGGTT CAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGCCATTCA CGCAGGGACCATCAAGTGCAACTTGCGGGG
TGCCTGGGTGATT CCTGGATCTCCCTGTTGATT CGGTGCTCCTGGGACCTTACCTGT
ACAGCATGTCTCTCGAAGACAAAGGTCTGGCAGAGGTGTCAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCAACACAGAGCCACCTAGTTGTCTTGTCAGCGC
CACGTGAGACACCTACAACGAGATGCCCTAACGCCAGCTCATGAATGCCCATCAGAAAGAA
GCTAAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTGTAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATAACCATGGGTCAAGGAGGC
GGTGGCGAAACTGAAGTGGCCAGAACTGCCCTAAATTCAAGCTGAAGTGGAAAGGCC
ACAGTGACCCCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTACTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTCTGCTTCTAAAAAAACCTAAGATTTTAAAAAAATTGAT
TTGTTTGATCAAATAAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELGKAEMIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGGGGAGAGGAGGCCATGGGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTGCGCATTGTGGGTGGAGAGGACGCCGACTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCCACTGCTTGAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCACCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTACACTAAACACATCCAGCCATCTGTCTCCAG
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCCTCCAGGAAGTCAGGTGCCATCATAAACAA
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG
GTTTGTGCTGGCAACGCCAACGGCGGGAGGATGCCTGCTCGGTGACTCAGGTGGACCCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCGGTGTCTACACCAATATCAGCCACCACCTTGAGTGGATCCAGAAG
CTGATGGCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTCCCTCT
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTTCTCTGTCTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLALLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAELGRWPWQGSLRLW
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGCRPNRPGVYTNIHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCACCGCGTCCGGACCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCCCGGAGCCCGACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGCCCCGGCGTGCAGGACCCCTGAGGAAGAGCTGAGTCTCACCTT
GCCCTGAGACAGCAGAAATGTGGAAAGACTCTCGGAGCTGGTGCAGGCTGTGTCGGATCCCAG
CTCTCCTCAATACGGAAAATACCTGACCCCTAGAGAATGTGGCTGATCTGGTGCAGGCCATCCC
CACTGACCCCTCCACACGGTGCAAAAATGGCTCTGGCAGCCGGAGCCCAGAAAGTGCCTT
GTGATCACACAGGACTTCTGACTTGTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTTCACTACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCCTGGCCCCCATGTGGACTTTGTGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCTGAGCCGCAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGTAACCCCCTGTGATCCGTAAGCGATAACAACCTGACCTCACAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCCCTGGAGCAGTATTCCATGAC
TCAGACCTGGCTCAGTTCATGCGCTCTCGGTGGCAACTTGACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAACAGGGCCGGGCCGGGATTGAGGCCAGTCTAGATGTGAGT
ACCTGATGAGTGTGGTGCACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGGCCCTTCCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGGCCCTACATCCAGCAGGGTCA
ACACTGAGCTCATGAAGGCTGCCGCTGGGTCTCACCCCTGCTCTCGCCTCAGGTGACAGT
GGGGCCGGGTGTTGGCTGTCTCTGGAAAGACACCAGTTCCGCCCTACCTCCCTGCCCTCCAG
CCCCTATGTACCACAGTGGAGGCACATCCTCCAGGAACCTTCCTCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCACGGCCTTCATACCAGGAG
GAAGCTGTAACGAAGTTCTGAGCTCTAGCCCCCACCTGCCACCATCCAGTTACTTCAATGC
CAGTGGCCGTGCTACCCAGATGTGGCTGCACCTTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCCATTCATGGGTGCCGGAACCTCGCCTCTACTCCAGTGTGTTGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTTGGCTTCTCAACCCAAG
GCTTACCAAGCAGCATGGGCAGGTCTTTGATGTAACCGTGGCTGCCATGAGTCCTGTC
TGGATGAAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGCTGGATCCTGTAACAGGC
TGGGGAACACCAACTCCCAGTTGCTGAAGACTCTACTCAACCCCTGACCCTTCCCTATC
AGGAGAGATGGCTTGTCCCCCTGCCCTGAAGCTGGCAGTTCACTCCCTTATTCTGCCCTGTTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA
TGCTGTGAGCTTGACTTCACTCCAAACCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTTTGATGCTCTCCCTCCGC
ATCTCATCTTCTCTTTCAATCAGGCTTTCCAAGGGTTGTATAACAGACTCTGTGCACTA
TTTCACTTGATATTCACTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT
TTCCTACCTGACATCCAGAAACAATGCCCTCCAGTGCACATCTCAATCTTGTGTTATG
GCCTTCCATCATAGTTGCCACTCCCTCTCCTACTTAGCTCCAGGTCTTAACCTCTG
ACTACTCTTGTCTTCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTG
TCCATTGTAGATTTGCTCTCAGTTACTCATTGTCCCCGGAAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATAACCTCAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRTLPPGVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTL ENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLLPGAEFH YVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLM SAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLF DVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GCCGCGCGCTCTCTCCGGCGCCACACCTGTCTGAGCGGCGCAGCGAGCGCGGCCGGC
GGGCTGCTCGCGCGGAACAGTGCTCGG**ATGG**CAGGGATTCCAGGGCTCCTCTTCCTTC
TTCTTCTGCTCTGTGCTGTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTTG
GCCTGCATACCGCCTCCCTGCGTCTGCCCCAGTCTACCCCTCAATTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCCAGTGTCTAAGGGAAC
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTTGGAAAGGACTTCCTGCTCAACTACCCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGGCACCCCTGGTGGCAGAGAACATGTCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAACGCTTGAGTGGCTTCTAAAGCCC
AAGTTAAAGATGGTGGTCGAGGGCCAACGACTCCACTTCAGCCATGCCAGCAGATGAA
ATTCAGTGGATCCGGGTGAAACGCACCCATGTGCCAAGGGTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACTCAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGTGAGCCCTCTGCTAACGAGCTGCCAGGGGAGAACATTCACTTCTC
TGGTTATGACAATGACCGACCAGGAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCTCTACCAGCAATGCGATGCCAGCCAGGGCCAGGGTCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAACGTTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG
TGACACAGTGTCCCTGGCAGCAATTAGGGTCTTCATGTTCTTATTTAGGAGAGGCC
AAATTGTTTTGTCTTGGCGTGCACACGTGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTACCTATTCTTACAATTGCAAGATGACTGGCTTACTATTGAAAATG
GTTTGTGTATCATATCATATCATTAAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTGGGCAATGAGGAATTGGACAATTAGTTAATCTTCACGTTTGT
CAAACTTGATTTATTCATCTGAACCTGGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRD
SGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHV
LTAACIH
DGKTYVKG
TQKLRVGF
LKP
KFKDGGRGANDSTS
AMPEQM
KFQWIRVKRTHV
PKGWIKGNANDIGMDYD
Y
A
L
LE
LKKPH
RK
KFM
KIGV
SPPAK
QLP
GGRIH
FSGYD
NDR
PGNLV
YRF
CDV
KDE
TYD
LLYQQCD
AQPGASGSGVYV
RMW
KRQQQ
KWER
KIIGI
FSGH
QW
VDM
NGSP
QDF
NV
AVR
ITPL
KYAQ
IC
YW
IK
GNY
LDC
REG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGGTCTCTGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGGTTT
CTGGAGCGCCCCCAGCCCTGGGTGGGGCTGTCTCGGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGCGGCCAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCAC TGCGCAGGTTCTGCTCACCAAGCCGCTGGGTGATC
ACTGCTGCCCACTGTTCAAGGACAACCTGAACAAACCATACTGTTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGAACCCCTGGCTCTGGTCCCAGAAGGTGGGTGTTGCCCTGGGTGGAGC
CCCACCCCTGTGTATTCTGGAAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCCTGCCATCTGCCTACCTGATGCCCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCCTCAGACCCCTGCAGAACAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCAGGGATGCTTGTCTGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCGGCATCATCAGCTGGGGCGAGGGCTGTGCCAGCGAACAGGCC
GGGGTCTACATCAGCCTCTGCGCACCGCTCTGGTGGAGAACGATCGTCAAGGGGTGCA
GCTCCCGGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCC
CCGCGCGCTCCTAGGGCGCAGCGGACGCCGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGCGGCCTCGGCGGTTCCCCCGCCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGCCAAACGCCCTCATGTCCCCGCCAC
GACTTCCGGCCCCGCCGGCCCGAGCGCTTTGTATATAATGTTAATGATTTTAT
AGGTATTTGTAACCCTGCCACATATCTTATTATTCCCTCCAATTCAATAATTATTATT
CTCCAAAAAAA

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI
PVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITA
AHCFKDNLNKPYLFVLLGAWQLGNPGSRSQKVGV
A
WVEPHPVYSWKEGACADIALVRLERSIQF
SERVLPICL
PDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPI
IDSEVC
SHLYWRGAGQGPITEDMLCAGYLEGERD
ACLGDSGGPLMC
QVDGA
WLLAGIISWGEGCAERNRPGVYISLSA
HRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTCTGATGCTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCCGGAGCCCTCACAGATGAGGAGAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGCCAC
AACAAAGGAGCGGGCGCCGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCCAGGCCAGATGTGGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC
GGCTGTGGTCCCACCTCTGTGAGAAGCTCCAGGTGTTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTTGCCTAACCTGGTAAC TGAGGCCCATCCTCCGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTCTCCCTAGCAACGGGATTCCGGCTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGAAACCCAGGCC
CCAACCTCCTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTGCGTAAC
AACTGAGGTCCCTCCATTGGCAGCTCACAGCCTGCCCTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCCAGAGAACTCTGGACCCCAAGATGTCCCTGACAGGGCAAG
GGAACCTCCTACCCATGCCAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCAGTG
AGGTCTTGGCCTCAGTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGTCCCTGCCAGGTGAGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGTCATGTGTGGGCCCTCCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCAACTCAAAGGG
TGAAGAGGTAGCTGTCCTCTGTCACTTCCCCACCCCTGTCCCCAGGCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGCATGTGCCCTCATCACACCCTCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCTCCTGCCCTCCCTGAGTCCTGGGGTGGAGGATTGAGGGAGCT
CACTGCCTACCTGGCCTGGGCTGTCTGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGGCCCACTGGAGTGGGTTTC
TTTGAGTGGGGAGGCAGGGACGAGGAAGGAAAGTAACCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLLPLLLL VATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKVPSRSPENS LDPKMSLTGARELLPHAQEEAEAEALPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAE GPDKPSVV
SGLNSGPGVWGPPLLGLLLPPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACGTGAAAGTCAGGCTTTCATTTGGGAAGCCCCCTAACAGAACCGGTCAATTCTCCAAGTTATGGTGGACGT
ACTTCTGTTCTCCCTCTGCTTTCACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTCAT
CAAGGCAAGTCCATGAGCCACCTCAAGCCTCGAGAAAGTGAACACTGAACAATGAATTGGAGACCATTCC
AAATCTGGGACAGTCTCGGCAAATATTACACTTCTCTCCTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
ACATCTGAAAGAGTTCACTGAAACTTTGGACCTTAGCAGAACAAATATTCAAGAGCTCCAAACTGCATT
TCCAGCCCTACAGCTCAAATATCTGTATCTCACAGCAACCGAGTCACATCAATGGAACCTGGTATTTGACAA
TTTGCCAACACACTCCTGTGTTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAAGATGTTAAACT
GCCCAACTGCAACATCTGAATTGAACCGAAACAAGATTAAAATGTTAGATGGACTGACATTCCAAGGCCTGG
TGCTCTGAAAGTCTGAAATGCAAAGAAATGGAGTAACGAAACTATGGATGGAGCTTTGGGGCTGAGCAA
CATGAAATTTGCACTGGACCATAACAACTAACAGAGATTACCAAGGCTGGCTTACGGCTTGCTGATGCT
GCAGGAACCTCATCTCAGCAAATGCCATCACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAAGCTCAG
TGAGCTGGACCTAACCTTCAACTTACATTCAAGGTTAGATGATTCAAGCTTCTGCCCTAAGCTTACTAAATAC
ACTGCACATTGGAAACAACAGACTCAGCTACATTGCTGATTGCTCTCCGGGGCTTCCAGTTAAAGACTTT
GGATCTGAAAGAACATGAAATTCCTGGACTATTGAAGACATGAATGGTGTCTCTGGGCTTGACAAACTGAG
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTCACTGGTTGGATGCAATTGGAGCA
TCTAGACCTGAGTGAACACGCAATCATGTCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAAATT
GCATTAAATACATCAAGCTTTGCGATTGCCAGCTAAAGGAAAGAAGCATTGGCTCCACAGTGGGTGGCGAAAACAACCT
TCAGAGCTTGAAATGCACTGTTGCTGCCCCATCCTCAGCTGCTAAAGGAAAGAAGCATTGGCTGTTAGGCCAGA
TGGCTTGTGTGATGATTTCACAGCTGCCAGCAGTGTGATTCCCCATGACTTTGCTTGGAAAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGGAAAATTATGCACACCTCCGGGCCAACGGTGGCAGGGTGTGAGTACAC
CATCCCTCGGCTGCGAGGTGAAATTGCCAGTGAGGGAAATACAGTGTGTCACTCCAATCATTGGTTC
ATCCTACTCTGCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACCAT
CCGAGCTGGGGCATGGCACGCTGAGTGTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA
TGGGGCACAGACTCCAGCTGCACGGAGAGACGCATGATGATGCCAGGGATGACGTGTTCTTATCGT
GGATGTGAAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTCAGGAAGTATTTCAGCAAATGC
AACTCTGACTGCTCTAGAACACCATCATTTCGCGGCCACTGTTGGACCGAATGTAACCAAGGGAGAAACAGC
CGTCTACAGTGCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAAACTGGACCAAAGATGATAGCCATTGGTGGT
AACCGAGAGGCATTTCGAGCAGGCAATCAGCTTCTGATTATGTGGACTCAGATGTCAGTGTGCTGGAA
ATACACATGTGAGATGCTAACACCCCTGGCACTGAGAGAGGAAACGTCGCGCCTCAGTGTGATCCCCACTCCAAC
CTGCGACTCCCCCTCAGATGACAGCCCCATCGTAGACGATGACGGATGGGCCACTGTGGGTGTCGTGATCATAGC
CGTGGTTGCTGTGTTGGCACGTCACTCGTGTGGTGTGATCATATACACACAAAGGGAGGAATGAAGA
TTGCAGCATTACCAACACAGATGAGACCAACTTGCAGCAGATATTCTAGTTATTTGTCATCTCAGGAACGTT
AGCTGACAGGCAGGATGGGTACGTGCTTCAGAAAGTGGAAAGCCACCAAGGTTGTCACTTCAAGGTGCTGG
ATTTTCTTACACATGACAGTAGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAGCTGC
CACAGATCTGTTCTTGTCCGTTTGGGATCCACAGGCCCTATGTATTGAAAGGAAATGTGTATGGCTCAGA
TCCTTTGAAACATATCATACAGGTTGCACTGCTGACCCAAAGAACAGTTTAATGGACCAACTATGAGCCCAGTTA
CATAAAGAAAAGGAGTGTACCCATGTTCTCATCCTCAGAAGAACCTGCCAACGGAGCTTCAGTAATATATC
GTGGCTTCACATGTGAGGAAGCTACTAACACTAGTTACTCTCACAAATGAAGGACCTGGAATGAAAATCTGTG
TCTAAACAAGTCTCTTGTGAAATGCAATCCAGAGCCAGCGTCGGTGCCTCGAGTAATTCTTCATGGG
TACCTTGAAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTCAGCC
AAGAGCCTTTATTGAAAGCTCATCTTCCCAAGACTTGGACTCTGGGTCAAGGAAAGATGGAAAAGAAAGGAC
AGATTTCAGGAAGAAAATCACATTGTACCTTAAACAGACTTTAGAAAATACAGGACTCCAAATTTCAGTC
TTATGACTTGGACACATGACTGAATGAGACCAAGGAAAAGCTTAACATACTACCTCAAGTGAACCTTATT
AAAGAGAGAGAATCTTATGTTAAATGGAGTTATGAAATTAAAGGATAAAATGTTTATTATACAGAT
GAACCAAATACAAAAGTTATGAAAATTTCATCTGGGAATGATGCTCATATAAGAACACCTTTAAACTA
TTTTTAACTTGTGTTATGCAAAAAGTATCTACGTAATTAAATGATATAATCATGATTATTTATGTATT
TTATAATGCCAGATTCTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCATTGACCAATT
TTAAATAGAAGTTACTTCATTATATTGACATTATTTAATAAAATGTGTCATTGAA

FIGURE 102

MVDVLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQLSLREVKLNNELETIPNLGPVSA
ITLLSLAGRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRIASAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMDGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAIRISPDWE
FCQKLSELDLTFNHLRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDDLKNNE
ISWTIEDMNGAFSGLDKLRRRLIQGNRIRSIKKAFGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQLKWLPPQWAENNFQSFVNASCAPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNEHHDAEMENYAHLRAGQ
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVAKLTNVMLPSFTKTPMDLTIRAGA
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFIVDVKIEDIGVYCTAQN
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPQLNWTKDDSPVVTER
HFFAAGNQLLIVDSDVSDAGKYTCMSNTLGETGNVRLSVIPTPTCDSPQMTAPSLLDDG
WATVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTLAD
RQDGYSSESSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEATDLFLCPFLGSTGP
MYLKGNVYGSDFPETYHTGSPDPRTVLMHDHYEPSYIKKKECYPCHPSEESCERSFSNISW
PSHVRKLLNTSYSHNEPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGTTGGGTGCCCTGCACAAAGGATGAGGATGCAGGACGCCAGCTTCTCTGGAACCGAACGCAATGGATAAAACTGATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTCTTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAATAACCAGAGTTAGACCCGCGGGGTTGGTGTCTGACATAAAATAATCTTAAAGCAGCTGTTCCCTCCCAACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCAAAAGAAAAAGTATGTTCATTTTCTCTATAAAAGGAGAAAGTGAAGCCAAGGAGATATTGGAATGAAAAGTTGGGCTTTTTAGTAAAGTAAAGAACTGGTGTGGTGGTGTTCCTTCTTTGAATTCCACAAAGAGGAGAGGAAATTAAATAATACATCTGCAAAAGAAATTCAGAGAAGAAAAGTGAACCGCAGATTGAGGCATTGATTGGGGAGAGAAACCAGCAGAGCACAGTTGGAATTGCGCTATGTTGACTAAAATTGACCGATAATTGCACTGGATTTCATCAACCTCCTTTTTAAATTTTTATTCCCTTGGTATCAAGATCATGCGTTCTCTTGTCTAACACACCTGGATTTCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACTGTTGAATTCCAAGGACCAACACCAGATAAAATTATGAATGTTGAAACAGATGACCTTACATCCACAGCAGATAATGATAGGTCTTAGGTTAACAGGGCCCTATTGACCCCTGCTTGTGGTGCCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGGGCTCAGACCTGCCCTCTGTGTGCTCTGCAGCAAACAGTTCAAGGATTTGTGTTGGGAAACCTCGCTGAGGGTCTGGGATGGCATCTCACCAACACACAGGCTGCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCAGTGGAGCACTTGGAAACCTCTAACAGTTGAGTAGGAACCATATCAGAACCATTTGAATTGGGGCTTCAATGGTCTGGCAACACTAACACTTGGAAACTCTTGACAAATGTCCTACTACCATCCGAATGGAGCTTGTATACTTGTCTAAACTGAAGGACCTCTGGTGGCAAACAACCCATTGAAAGCATCCCTTCTTATGCTTTAACAGAACTCCTTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTCATACATCTCAGAAGGTGCCTTGAAGGTCTGTCAACTTGAGGTATTGAAACCTTGCATGTGCAACCTCGGAAATCCCTAACCTCACACCGCTCATAAAACAGATGAGCTGGATCTTCTGGGAATCATTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTGATGCACCTTCAAAACTGTGGATGATACAGTCCCAGATCAAGTGAACCGGAATGCCCTTGACAAACCTCAGTCAGTGGAGATCAACCTGGCACACAATAATCTAACATTACTGCCATGACCTCTTCACTCCCTGACATCTAGAGCGGATACATTACATCACAAACCTTGGAACTGTAACGTGACATACTGTGGCTCAGCTGGGATAAAAGACATGGCCCCCTGAACACAGCTTGTGCCCCGGTTAACACTCCTCCAACTCTAAAGGGAGGTACATTGGAGAGCTGACCAGAATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGTGGCTGAATGTCGGGCTCCACATCCTGACATCTGTATCTGGATTACTCCAAATGGAACAGTCATGACACATGGGGCTACAAAGTGCAGGATAGCTGTCCTAGTGTGGTACGTTAAATTCTACAAATGTAACGTGTGCAAGGATACAGGCATGTACACATGTATGGTGAAGTAACTCGTGGGAATACTACTGCTTCAAGGCCCTGGAATGTTACTGCGAGCAACCACTACTCCCTTCTCTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCAACGGGACACAGATAACAAATGTGGGCTCCACTCCAGTGGTCAGTGGAGACCAACCATGTCAGTGTGATATAAACAGTGGGATCCCAGGAATTGTGAGGTCTGAAGACTACCAAAATCATCATGGGTGTTTGTGCCATCACACTCATGGCTGCAGTGTGATGCTGGTCTTCTACAAAGATGAGGAAGCAGCACCATGGCAAAACCATCACGCCCAACAGGACTGTGAAATTATTAAATGTGGATGATGAGATTACGGGAGACACACCAGTGGAAAGCCACCTGCCATGCTGCTATGAGCATGAGCACCTAAACTACTCATACAAATCTCCCTCAACCAACAAACAGTTAACACAAATAATTCAATACACAGTTCACTGCAGTGCATGAAACGTTATTGATCGAATGAACTCTAAAGACAATGTACAAGAGACTCAAAATCTAAACATTACAGAGTTACAAAAACAAACAAATCAAAAAAAAGACAGTTATTAAAAATGACACAAATGACTGGCTAAATCTACTGTTCAAAAAAGTGTCTTACAAAAAAACAAAAAGAAATTATTATTAAATCTATTGTGATCTAAAGCAGACAAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFNRLTTIPNGAFVYLSKLKELWLRLNNPIESIPSYAFNRIPLSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDDELDSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLPHDLFTPLHHLERIHLHHNPWCNCDIL
WLSWWIKDMAPSNTACCACRNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVNSVGN
TTASATLNVTAAATTFSYFSTVTETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYN SYKSPFNHTTVNTINSIHSS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGRGELGQPSGVAERPCPTTCRCLGDLDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLILNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRISSAIIPPKMFKLQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC
QKLSELDLTFNHLSRLDDSSFLGLSLLNLTIGNNRVSYIADCAFRLGSSLKTLDLKNNEIS
WTIEDMNGAFSGLDKLRRLILQGNRIRSIKAKFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQQLHLNTSSLLCDCQLKWLPOQVAENNQSFVNASCAPQLLKGRSIFAVSPDGVCDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVAKLTNVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCAQNSA
GSISANATLTVLETPSFLRPLLRTVKGETAVLQCIAGGSPPPKNWTKDDSPLVVTERHF
FAAGNQLLIIVDSVDAGKYTCMSNTLTERGNVRLSVIPTPTCDSPQMTAPSLLDDGWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTLADRQ
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKGNVYGSDPFETYHTGSPDPRTVLMHDYEPSYIKKKECYPCHSEESCRFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLDGSSEEDGKERTDFQEENHICTFKQTLERYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTCGGGAGAGCGCCAGCTGACTTGAATGGAAGGAGCCCAGGCCGGAGCGCAGCTGAGAC
TGGGGGAGCGCGTTCGGCCCTGTGGGGCGCCGCTCGGCCGGGGCGCAGCAGGAAGGGAAAGCTGTGGTCTGCC
CTGCTCCACGAGGCAGCCACTGGTGTGAACCGGGAGAGCCCTGGTGGTCCCGTCCCTATCCCTCTTATATA
GAAACCTTCCACACTGGAAAGGCAGGGCAGGAGGGCTATGGTGAGCAAGGAGGCCGCTGATCTGAG
GCGCACAGCATTGGAGTTACAGATTTACAGATACCAAATGGAAGGCAGGGAGGCAGAACAGCCTGCC
TCCATCAGCCCTGGCGCCAGGCAGCTGACTCGGCACCCCTGCAGGCACCATGGCCAGAGGCCGGGTGCTGC
TGCTCCTGCTGCTGCTGCCACAGCTGCACCTGGGACCTGTGCTTGCGTGAGGGCCCAAGGATTGGCCGAA
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTGCGGAGGGAGGCCGTGCTGTTACTGAGCCCTGAGG
AGCCCGGGCTGGCCAGCCGCGGTAGCTGCCCGAGACTGTGCCCTGTTCCAGGAGGGCGTCGGACTGTG
GCGGTATTGACCTGCGTGAAGTCCCCGGGGACTGCGCTGAGCACACCAACCACTATCTCTGCAGAACACACCAGC
TGGAAAAGATCTACCCCTGAGGAGACTCCCGGCTGCACCCGGCTGGAGACACTGAAACCTGAAAACAAACCGCCTGA
CTTCCCAGGGCTCCAGAGAACGGCTTGAGCATCTGAGAACCTCAATTACCTGACTTGGCCAATAACAAGC
TGACCTTGGCACCCGCTCCTGCCAACGCCCTGATCAGTGTGGACTTTGCTGCCAACTATCTCACCAAGATCT
ATGGGCTCACCTTGGCCAGAACGAAAATTGAGGTCTGTGACCTGCACAAACAAGCTGGCAGACGCCGGGC
TGCGGACACATGTTCAACGGCTCAGCAAGCTGAGGTCTCATCCTGTCAGCAACTTCCGCCACGTGC
CCAAGCACCTGCCGCTGCCCTGACAAGCTGACCTCAAGAACAAAGCTGGAGAAGATCCCCGGGGCCT
TCAGCGAGCTGAGCAGCCTGCGCAGCTATACTGCAGAACAAACTACCTGACTGACGAGGGCTGGACAACGAGA
CCTTCTGGAAGCTCTCAGCCTGGAGTACCTGGATCTGTCAGCAACAAACCTGTCGGGTCCCAGTGGCCTGCCGCGTGC
CGCGCAGCCTGGTCTGCTGCACCTGGAGAACGACCGCATCCGGAGCGTGGACCGAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGCTGCACAGCAACCAGCTGCCAGCAGGGCATCCACCCACTGCCCTCCAGGGCC
TCAAGCGGTTGCACCGTGCACCTGTACAACAACCGCCTGGAGCGCTGCCAGTGGCCTGCCGCGTGC
GCACCCCTCATGATCCTGCACAACCAGATCACAGGCAATTGGCGCGAAGACTTGCACCCACTACTCCTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACAGGCCACAGGTGCACCGCAGCCTCCGCAAGCTGCCCTGCTGC
GCTCGCTGGACCTGTCGGCAACCGCTGCACACGCTGCCACCTGGCTGCCCTGAAATGTCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGCTGCCCTGGCACAGAGGGCGCTGGCGGATGGCTCAGCTGCGTGAGCTGTACCTCA
CCAGCAACCGACTGCGCAGCCCTGGGCCCGTGCCTGGTGGACCTGCCCATCTGCAGCTGCTGGACA
TCGCCGGAAATCAGCTCACAGAGATCCCCGAGGGCTCCCGAGTCACTTGAGTACCTGAGAACAAACA
AGATTAGTGCCTGGCCGCAATGCCCTCGACTCCACGCCAACCTCAAGGGATCTTCTCAGGTTAACAAAGC
TGGCTGTGGCTCCGTGGACAGTGCCTCCGGAGGCTGAAGCACCTGCAAGGTCTTGACATTGAAGGCAACT
TAGAGTTGGTGCACATTCCAAAGGACCGTGGCCGCTGGAGAACAAAGGAGGAGGAGGAAGAGGAGGAGGAGG
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGGGACTTTCTGC
AGCACACGCCCTGTGCTGTGAGCCCCCACTCTGCCGTGTCACACAGAACACCCAGCTGCACACATGAGGCA
TCCCACATGACACGGCTGACACAGTCTCATATCCCCACCCCTCCACGGCGTGTCCCACGCCAGAACATGC
ACACACATCACACCCCTCAAACACCCAGCTCAGCCACACACAACACTACCCCTCAAACCCACACAGTCTGTACAC
CCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAGGGCTGCCCTGGCACACACAGGCCACCA
TCCCTCCCCCTGCTGACATGTGATGCGTATGCATACACACCACACACACATGCACAAGTCATGTGCGAA
CAGCCCTCCAAAGCTATGCCACAGACAGCTTGCCTGCCAGCCAGAACATGCCATAGCAGCTGCCGTGCC
GTCCATCTGCCGTCCGCCCTGGAGAACACACAAGGTATCCATGCTGTGGCCAGGTGCCACCCCT
GGAACTCACAAAAGCTGGTTTATCCTTCCATCCTATGGGGACAGGCCCTCAGGACTGTGGCCTGGCC
TGGCCACCCCTGCTCCCTCAGGTGCTGGCGAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCAGTTTCCAATGGCAAGCCCAGTGGAGGCAGGATGGGAGAGGCCCTGGGTGCTGCTGGGGCTTGGGG
CAGGAGTGAAGCAGAGGTGATGGGGCTGGGTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTT
GTTCTCAGGCCTGTGGGGAAAGTCCGGGTGCTTATTTTATTCTTCTAAGGAAAAAAATGATAAAAAT
CTCAAAGCTGATTTCTTGTATAGAAAACATAATAAAAGCATTATCCCTATCCCTGCAAAAAAA

FIGURE 108

MEGEEAEQPAWFHQFWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENEFAEEEPVLVLSPEEPGPAAVSCPRDCACSQEGVVDGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRLHRLETLNLQNNRLTSRGLPEKAFEHTNLNYLYLANNK
LTLPAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLISSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPDRVTLMILHNQITGIGREDFATTYF
LEELNLSYNRITSQPVHRDAFRKLRLRSRDLGNRLHTLPPGLPRNVHVLKVKRNEALAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKIGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

FIGURE 110

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGC DVVKGQIRCQCPSPGLHLAPDGRTCDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDL MYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNIPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTT PERPTTGLTTIAPA AASTPPGGITVDN
RVQTDPQKPRGDVF SVLVHSCNFDHGLCGWI REKDNDLHWEPI RD PAGGQYLT VSAAKAPGG
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACTTCCCTTGCAACAGGTGCTGCTGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCA
ACAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTCTGACTTGAATACC
AACACAAGTCACCATGATGCCACCCAATGCATCTGCTTATCAACCCACTGCAGTTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAAGGAAATGGAACACTATCTGCCAGTCA
GAAGATAACAAGTCACGGTTGATGATCCTGTACAAAGCCAGTGGTGCAGATTCATCCTCCCT
CTGGGGCTGTGGAGTATGTGGGGACATGACCCCTGACATGCCATGTGGAAGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTT
TCCCCAAAACAATACCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGAATTACAGCT
GCCTGGTGAGGAACCCGTCACTGAGTAAATGGAAAGTGATATCATTATGCCCATATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAGTAGGGGAAGTGTACTGT
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGGCCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGCTTACAACAACATAAC
CGGCAGGCAAGATGAAACTCATTTCACAGTTATCATCACTCCGTAGGACTGGAGAAGCTG
CACAGAAAGGAAAATCATTGTCACCTTAGCAAGTATAACTGGAATATCACTATTTGATT
ATATCCATGTGTCTTCTCTTCTATGGAAAAAATATCAACCCTACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAACAGAACATACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTCGGAATATATGAATTGTTGCTTCCAGATGTTCTGGTGTTCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATGGGCAAGATTGCACAGTACAGT
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATTCAAGAGTGAACCTTCATGG
GCTAAACAGTACATTCAAGTGAAGAAATTCTGAAGAAACATTAAAGGAAAACAGTGGAAAAGT
ATATTAAATCTGGAATCACTGAGAAGAAACCAGGACCAACACCTCTACTCATTATCCTTACA
TGCAGAACAGGACATTATGCAAATTGAACCTGCAGGTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAACATGTTGGGAAATATTCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGTTCCATAAGTTGTATGAAATATCTACAAACCTCA
ATTAGTTCTACTCTACACTTCACATCAACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAAACTTTACATTGTTGATTTTCAGCAGACTTTGTTTATTAAATTGTTATTAGTG
TTAAGAATGCTAAATTATGTTCAATTATTCCAAATTCTATCTTGTATTGTACAA
CAAAGTAATAAGGATGGTTGTCAAAAAACAAAACATGCCTCTCTTTTTTCAATCACC
AGTAGTATTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTTA
TTTTTTCAAGGAAAGATGGATTCAAATAATTATTCTGTTTGTAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQI IWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPIVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRSPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTGCAGTCCCCGGCAGTCCTGGCTT
GCTTGGGGTGCTCCCTGGACGCACGGCGGGAGCAACGTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTATGCCCGTGGTGCCTGCT
TGTCAAAATCTCAACCGGAATGGGAAAGTTGCTGAATGGGGAGAAGATCTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTATCATTGTAAGATGGTGAATTAGGCCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAAACTTATAAGTATAAAGAGTGGAAAGAGTATTGAGCCGTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTTATTGAAGACCTGGATTGCCAGTGTGGGATCATATACT
GTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC
AGATTGCCTTGTCCCTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTCAAAAAAAAT
TATTATCAGAACATCTGCACAACCTTGAAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTTCCACAGAACATGC
CATAAAGACAACGCTCTGGTCCATCATTGCCACAGATAAAATCTAGTTTAAATTATAG
TTATCTTAATATTATGATTTGATAAAAACAGAACAGATTGATCATTGTTGGTTGAAGTG
AACTGTGACTTTTGAAATATTGCAAGGTTCTAGCTAGATTGTCATTAAATTGAAGAGTCTA
CATTCAAGAACATAAAAGCACTAGGTATACAAGTTGAAATATGATTTAACAGTATGATG
GTTTAAATAGTTCTCTAATTGAAAAATCGTGCACAGCAATAAGATTATGATATTGTT
TTAATAATAAACCTATTCAAGTCTGAGTTGAAAATTACATTCCCAAGTATTGCAATTAT
TGAGGTATTAAAGAAGATTATTAGAGAAAAATTTCCTCATTTGATATAATTTCCTCTG
TTTCACTGTGAAAAAAAGAAGATATTCCATAAAATGGGAAGTTGCCATTGTCTCAAG
AAATGTGATTTCAGTACAATTCTGTTCTTTAGAGGTATATTCCAAATTTCCTTG
ATTTTAGGTTATGCAACTAAACACTACCTACATTAAATTACAGTTCTACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTAAGTTCATGGTATTCTCTGATT
CAACAAAGTTGATTTCTCTGATTTTCTTACTTACTATGGGTTACATTTCATT
CAAATTGGATGATAATTCTTGAAACATTTCATTGTTAGTAAACAGTATTTCATTGTT
GTTTCAAACGTGAAAGTTACTGAGAGATCCATCAAATTGAAACATCTGTTGAATTAAAATT
TTGCCACTTTTCAAGATTACATCATTCTGCTGAACCTCAACTGAAATTGTTTTTT
TTTCTTTGGATGTAAGGTGAACATTCTGATTGTTCTGATGTAAGGGCTGGTA
TTTACATTGAAAATTCAAAGAAGCTTAATATAAAAGTTGCATTCTACTCAGGAAAAAG
CATCTCTGTATATGCTTAAATGTATTTGTCCTCATACAGAAAGTTCTTAATTGAT
TTTACAGTCTGTAATGCTTGATGTTAAAATAAACATTTCATTTCATT
ACTTCATATTATCCTGTGTTCTTCCTGACTGGTAATTGTTGTTGGATTTCACAGGTA
GTCAGTAGGATGGAACATTAGTGTATTTCATTCTAAAGAGCTAGAATACATAGTTT
CACCTAAAAGAAGGGGGAAATCATAAAATACAATGAATCAACTGACCATTACGTAGTAGAC
AATTCTGTAATGTCCTCTTCTAGGCTCTGTTGCTGTGAATTCCATTAGATTACAG
TATCGTAATATACAAGTTCTTAAAGCCCTCTCCTTAAAGAATTAAAATTGTA
AAAGAGTTGGATGTTGTAACCTGATGCCATTAGAAAAATATCCTAAGCACAAAATAACCT
TTCTAACCACTCATTAAAGCTGAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPYPSKKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCAGTGTCCAGCTGGAGACCGTATAATTGTTAACTAATTCAACAAACGGGACCCCTTCTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGACAGGCGGATTGGAAGAGCGGGAAAGTCCTGGCCAGAGCAGTGTGACACTTCCTCTGTGACCATGAAACTCTGGGTGTCTGCATTGCTGATGGCTGGTTGGTGTCTGAGCTGTGAGGCGAATTCTTCACCTCTATTGGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATCCTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGACTAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGGTGAAGCGGCTAAACACAGACTGGCTGCGCTGGAGGACCTTGTGCTGAGGACTCAGCTGCAGGTTTATGCCAACCTCTCTGTGAGCGGAGTTCTCCCCACTGATGAGGACGGAGATAGGAGCTGCCAACAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCAAGGGGAACCTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATGGCGCTCGGAGGACAGGTGCTAAAGCAGCTTGATGCCGGGGAGGAGGCCACCAACCAAGTCACAGGTGCTGGACTACCTCACTATGCTGCTTCCAGTTGGGTGATCTGACCGTGCCTGGAGGCTCACCGGCCCTGCTCTCCCTGACCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTGAGCAGTTATTGAGAAGAGAGAAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAGGCAACTATGAGAGGCCTGTTGGACTACCTGCTGAGAGGGATGTTACGAGAGCCTCTGCTGGGAGGGTGTCAAACACTGACACCCCTAGACAGAAGAGGCTTCTGTAGGTACCAACATGGCAAACAGGGCCCCACAGCTGCTCATTGCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACAACGTCAGGTACTACGATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAACCTAAACTGCACGAGCCACCGTTGATCCAAAGACAGGAGCCTCACTGTCGCCAGCTACCGGTTTCAAAAGCTCCTGGCTAGAGGAAGATGATGACCCCTGTTGTGGCCCGAGTAAATCCTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCGAGATTGTTACAGGTTGCAAATTATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTGACAGCGGCCCTAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTGAGGGTGCCTCTTGTGGGCTCTTGTGAGGAGGACAGTGGCTTCAAGAAGGGTACAGCTGTGTTCTGGTACAACCTCTTGCGGAGCGGGGAAGGTGACTACCGAACAAAGACATGCTGCCCTGCTGCTGAGGAGGTTCTGAGGACCTTGTGGATCAACAGAGTTGACTGACATCCTTTCTGTCCTTCCCTCCTGGTCCTCAGGCCATGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCTGATTGGAGGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGTGACTGAAGTCCCAGCCCTTCCATTAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCAAAAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTGTTTACGGTGTGAGATGTTCAAGAACAAAGTTCTGATAACCTTGTGTTACATGTTGTTTATGGCATTCTATCTATTGTGGCTTACCAAAAAATAAAATGTCCTACCAAGAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGEELPGTKYQAMLSVDDCFGMGRSAYNEGDDYYHTV
LWMEQVLKQLDAGEEATTKSQVLQDYLQYAVFQLGDLHRALELTTRRLSLDPSHERAGGNLR
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVDPYPERDVYESLCRGEVQLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYYDVMSSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAIWPKKGTAVFWYNLLRSGEVDYR
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTCCTCTTTAGTGGAAAGACAGACCATATACTCCAGTGTGAGTGAAATTGATTGT
TTCATTTATTACCGTTTGGCTGGGGTTAGTTCCGACACCTTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA
AGACAGGACAATCTTCTGGGATGCTGGTCTGGAAAGCCAGCGGGCCTGCTCTGTCTTGGCCTCATTGACCC
CAGGTTCTCTGTTAAACTGAAAGCCTACTACTGGCCTGGTGCCTCAATCATTGATCCTTGAGGCTGTGCC
CCTGGGCACCCACCTGGCAGGGCTACCACCATTCCGACTGAGCTCCCTGTTGGCTCTGCTGCAGGCCAGCGCTTC
CCCTCATCTTAGGGCTGTCCTGGGGTGAGCCTGAGCCTGAGCTGGGGTTCTGGATCCAGGGGAGGGAGAAG
ATCCCTGTGTGAGGCTGTAGGGGAGCGAGGAGGCCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG
ATGAAGACTTCAAACCCCGATTGTCCCCTACTACAGGGACCCACAAGCCTACAAGAAGGTGTCAGGACTC
GGTACATCCAGACAGAGCTGGGCTCCGTGAGCGGTTGCTGGTGGCTGACCTCCGAGCTACACTGTCCA
CTTGGGCTGGCTGTGAACCGTACGGTGGCCATCACTTCCCTCGGTTACTCTACTTCACTGGCAGCGGGGG
CCCAGGCTTCCAGCAGGGATGCAAGGGTGTCTCATGGGATGAGCGGCCGCTGGCTCATGTCAGAGACCCCTGC
GCCACCTTCACACACACTTGGGGCCACTACGACTGGTCTTCATCATGCAAGGATGACACATATGTGCAGGCC
CCCGCCTGGCAGCCCTGCTGGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGCAGAGGAGTTCATTG
GCGCAGGCAGGCCGGTACTGTCACTGGGGCTTGGCTACCTGTGACGGAGTCTCTGCTTCGCTTCGTC
GGCACATCTGGATGGCTGGCAGGGAGACATTCTCAGTGGCCGTCTGACGAGTGGCTTGGACGCTGCCCTCATTG
ACTCTCTGGGCGTGGCTGTCTCACAGCACAGGGCAGCAGTATGCTCATTTGAACCTGGCCAAAATAGGG
ACCCGTAGAAGGAAGGGAGCTGGCTTCTGAGTGCCTTCGCGTGCACCCGTCTCCGAAGGTACCCCTCATTG
ACCGCCTCCACAAACGCTCAGCCTGAGTTGGAGCGGGCTTACAGTGAATAGAACAACTGCAGGCTCAGA
TCCGGAACCTGACCGTGTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCGTTGGCTCCCTGCTCCTTCA
CACACACTCTGCTTGAGGTGCTGGCTGGACTACTTCACAGAGCAGCACACCTCTCCTGCAAGATGGG
CTCCCAAGTCCCACACAGGGGCTAGCAGGGCGAGCTGGTGTGCTGGAGACTGCCCTGGAGCAGCTCA
ATCGCGCTATCAGCCCCCTGCGCTTCCAGAACGAGCAGCGACTGCTCAACGGTATCGGCCCTGACCCAGCAC
GGGCATGGAGTACACCCCTGGACCTGCTGTGGAATGTGTGACACAGCGTGGCACCGGGGGCCCTGGCTCGCA
GGGTCACTGCTGCGGCCACTGAGCCGGTGGAAATCTACCTATGCCCTATGTCAGTGGCCACCCGAGTGC
AGCTGGTGTGCCACTCTGGTGGCTGAAGCTGCTGCAAGCCCCGGTTCTCGAGGCCTTGCAAGCCAATGTC
TGGAGCCACGAGAACATGCTACCCCTGTTGCTGGCTACGGCCACGAGAACGGTGGCCGTGGAGCTCCAG
ACCCATTCTGGGTGAAGGCTGCAAGCAGCGAGTTAGAGCAGCGTACCTGGACGAGGCTGGCTGGCTCG
CTGTGCGAGCAGGCCCTTCCAGGTGCGACTCATGGACGTGGCTCGAAGAACGACCCCTGTGGACACTCT
TCTCCTTACACCGTGTGGACAAGGCCCTGGGCCGAAGCTCTCAACCGCTGCGCATGAATGCCATCTGGCT
GGCAGGCCCTTCCAGTCCATTCCAGGAGTTCAATCTGCCCTGTCACCCACAGAGATCACCCCAAGGGCCC
CGGGGGCTGGCCCTGACCCCCCTCCCTGGCTGACTACCTGGCGGCCGAGCCCGTGGCAGGTGAAC
ACCGGCAGGCTCTGCGGAGGGCTGTTCTACAACGCTGACTACCTGGCGGCCGAGCCCGTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGCTGGAGGTGATGGATGTTTCTCCGGTCTCAGGGCTCC
ACCTCTTCGGCCGTAGAGCCAGGGCTGGTGCAGAACATTCTCCCTGGAGACTGCAGCCCCAGGCTCAGTGAAG
AACTCTACCAACCGCTGCCCTCAGCAACCTGGAGGGCTAGGGGCCGTGCCAGCTGGCTATGGCTCTTTG
AGCAGGAGCAGGCCAATAGCACTAGCCCCTGGGGCCCTAACCTCATTACCTTCTGTCTGCCAGCC
CCAGGAAGGGCAAGGCAAGATGGTGACAGATAAGAGAATTGTTGCTGTATTTTAAATATGAAAATGTTATTAA
ACATGTCTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD
QSDEDFKPRIVPYYRDPNKPYKKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRPHLDGCRG
DILSARPDEWLGRCLIDS LGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPGEAGLSWPVGLPAPFTPHSRFEV
LGWDYFTEQHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMEYTLDLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVPLLL
VAEAAAAPAFLEAFAANVLEPREHALLTLLVYGPREGGRGAPDPFLGVKAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPGPEVLNRCRMNAISGWQAFFP
VHFQEFPALSPQRSPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEEALEGLEVMVDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRAGQLAMALFEQEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGC~~CC~~ACGTGAGAGGAACCGTGC~~GG~~CTGCCTT~~CC~~GT~~CC~~CAAGCC
GTTCTAGACG~~GG~~AAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTGG
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGCTGCAGTAAAGGAGACTGGACAAACACTGTGACAAAGCAG
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCAATTAAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCC~~TT~~GATAAGTATAGAGACCAATACA~~CT~~G
GTTCTCCTGCACGCC~~CC~~ACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGC~~TT~~CTATCTAGGCCACACTATAAAATCTGGAGACCTTGAAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGC~~TT~~CT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTAATACCAAACTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC
CAACCAGGTAGTAGAAGGCTGTTAGATGGCTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGTGATGGGTATACCGC~~TT~~AGGGCATTGGCATTTCAAT
GATGCATTGGTTTCTTACCTCAAATGGCTGACAATGACTGAGAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTTGTCATTATTGTAGTAGTAACATACATACCAAA
TACAGCTGTATGTTCTTTCTTCTAATTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAAACACATGAACATTGAAATG
TGTTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAATAACTATTAAATAATTATAT
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTGCTGATTGGTT
AAAAAAATTAAACAGGTCTTAGCGTTCTAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAAACCTTAGCTGTGTTCCCTTACTCTAATACTGATTATGTTCT
AAGCCTCCCCAAGTCCAATGGATTGCCTCTCAAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAGTGTAAAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAFFSSENVKFESINMDTNMDWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCNYGSGSVKNCCPLNWEYFQSSCYFFSTDТИWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFFIGLSDQVVEGQWQVVDGTPLTKSLSFWDVGEPNNIATLEDATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

09909200-021801

FIGURE 123

GGGACTACAAGCCCGCCGCGCTGCCGCTGGCCCTCAGCAACCTCGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCGCTCGGCTGCTGACTTCTTCTGCTGCTGCTTCAAGGGCTGCTGATAGGGGCTGTAATC
TCAAATCCAGCAATCGAACCCCAGTGGTACAGGAATTGAAAGTGTGGAACTGTCTTGATCATTACGGATTCCG
AGACAAAGTGACCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGTCTGAGAAAATCTGGGAAGACATCCCTGAAGATCTGAAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTGAGGTCGTTGCTGAAATGACCGAAGGAAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGAACCTGCTGTAGAGTGGCAAGGCTGTACCAAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCAACTGCCACGGATT
CCAGAGCCAATCCCAGATTGCAATTCTTCCACTTAAACTCTGAAACAGGCACCTTGGTGTACTGCTG
TTCACAAGGAGCACTCTGGCAGTACTACTGCATTGCTTCAATGACCGAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGTTCTGGTTGCTCTGTTACTGGCCCTG
TCACGTGGCATTGCTGTGCATACAGACGTGGCTACTTCATCAACAAATAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACCGAGATGGAGTTAACATCCGCACTGACGAGGAGGGCAGTTCAAGACACAAGTCATGTTTG
TGATCTGAGACCCCGCGGTGAGGCGCACAGAGCGCACGTGACATACCCCTGCTAGAAACTCCGTCAA
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTAGAAAGCTTTGTTGGCCAAAGTTGACCA
CTACTCTTCTTACTCTAACAGCCACATGAATAAGAAAGATTTCCTCAAGATGGACCCGGTAAATATAACCCACAA
GGAAGCGAAACTGGTGGCTCACTGAGTTGGTCTTAATCTGTTCTGGCCTGATTCCCGCATGAGTATTAGG
GTGATCTAAAGAGTTGCTCACGTAACGCCCGTGTGGCCCTGTGAAGCCAGCATGTTCAACACTGGTGT
CAGCAGCCACGACAGCACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCGGCGGAACCCA
GAAAAGGCTTCTTACACAGCAGCCCTTAATCTCATCGGCCCCAGACACCCAGCAGTTCTTAAAGGCTCTGC
TGATGGTGTGCACTGTTGAGGAAAGCTTTGGATCAGGATTGGTAAAGGAAACACCCAAATCAGGAAG
GTAAATTGGTGTGCAAGAGGGATCTGCTGAGGAACCCCTGTTGCTCAACAGGGTGTCAAGGATTAAAGGAA
ACCTTCGTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTCTATGGGTTGTTTATTTATAAAATT
TACATCTAAATTGCTAAGGATGTATTGATTATTGAAAAGAAAATTCTATTAAACTGTAATATATTGT
CATACAAATGTTAAATAACCTATTGTTAAAAGTTCAACTTAAGGTTAGAAGTTCAAGCTACTAGTGT
TGGAAAATATCAATAATTAGAGTTTACCCAAAGGAATCCCTCATGGAGTTACTGTGATGTTCTTTCT
CACACAAGTTTAGCCTTTTCAAAAGGGAACTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAATCCAGTTAAGCAATGTTGAAATCAGTTGATCTCTTCAAAAGAAAACCTCTCAGGTTAGCTTGA
GCCTCTCCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAAGCCCTCAGATGTACATACAGATG
CCAGTCAGCTCTGGGTTGCGCCAGGCAGGGCTCTAGCTCACTGTTGCCCTGCTGTCGCCAGGAGGCC
GCCATCCTGGCCCTGGCAGTGGCTGTGCTTCAAGGGCTCTGCTCATCCAGCACAGC
TCTCAGGTGGCACTGCAGGGACACTGGTGTCTCCATGTAGCGTCCAGCTTGGCTCTGTAACAGACCTCT
TTTGGTTATGGATGGCTCACAAATAGGGCCCCAATGCTATTGTTTAAGTGTGTTAATTATTGTT
AAGATTGTCAAGGCCAAGGCAATTGCGAAATCAAGTGTCAAGTACAATAACATTGTTAAAAGAAAATGGAT
CCCACGTGCTCTTGTCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGCGATTTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCTTTAAAGAACGTCAAGGTGGAGCAGCAGGCCAGGTGAAAGGCC
TGAAACGCCCTGAATCAAAGCAGTTCTAATTGACTTTAAATTGTTCATCCGCCGGAGACACTGCTCC
TGTGGGGGGACATTAGCAACATCACTCAGAAGCCTGTTCTCAAGGAGCAGGTGTTCTCAGCCTCACATGCC
GCCGTGCTGGACTCAGGACTGAAGTGTGTTCAAGGAGCAGTGTGAGAAGGAGCACTCCACTGTGCTG
GAATGGCTCTCACTACTCACCTGTCTTCAAGGAGCAGTGTGAGAAGGAGCACTCCACTGTGCTG
AATTGCAACATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGGCAGGCCCTGGCAGAGGCC
GGAAATGCTCCAGCAGTGGCTCAGTGTCCCTGGTGTGCTGAGGAGGATGGCTCCACCTGGGATT
CCTCCATCATTGCCACCTTGTAGAGAGGGATGGCTCCACCTGGCAGTGTGGGATT
TCTTGGTTGTCATAGTGTAGGGTAGGCTTATTGCCCCCTTCTTATACCCCTAAACCTCTACACTAGTGC
TGGGAACCCAGGCTGAAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGTTAAGATATGAATGTGACTCAAGACTCGAGGCCAGAGGCTGTGATTCT
GCCTTGGATGGATGTTGCTGACACAGATGCTACAGACTGTACTAACACACCGTAATTGGCATTGTTAAC
CTCATTATAAAAGCTTCAAAAAACCCA

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267